

# STIC Search Report Biotech-Chem Library

#### STIC Database Trade to

TO: Minh-Tam Davis

Location: REM-3A24&3C18

Art Unit: 1642

Friday, April 29, 2005

Case Serial Number: 09/674237

From: Toby Port

**Location: Biotech-Chem Library** 

**REM1-A59** 

Phone: 272-2523

toby.port@uspto.gov

#### Search Notes

Dear Examiner Davis,

Here are the results of your search.

Please feel free to contact me if you have any questions.

**Toby Port** 

proty 02/99 04/98



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### 151838

#### STIC-Biotech/ChemLib

From:

Chan, Christina

Sent: To: Subject:

Wednesday, April 27, 2005 12:34 PM Davis, Minh-Tam; STIC-Biotech/ChemLib RE: Rush search request for 09/674237

Please-rush. Thanks Chris.

Chris Chan

TC 1600 New Hire Training Coordinator and SPE 1644 (571)-272-0841 Remsen, 3E89

MIE

-----Original Message-----

From:

Davis, Minh-Tam

Sent:

Wednesday, April 27, 2005 12:31 PM

To:

Chan, Christina

Subject:

Rush search request for 09/674237

Please search in commercial database, issued patent files, and PGPUB:

1) A nucleotide sequence encoding SEQ ID NO:3, with size limitation of the sequences in the database 100 nucleotides or less.

2) SEQ ID NO:1, with size limitation of the sequences in the database 100 nucleotides or less. 3) SEQ ID NO:2, with size limitation of the sequences in the database 100 nucleotides or less.

Thank you. MINH TAM DAVIS

ART UNIT 1642, ROOM 3A24, MB 3C18

272-0830

*****	************					
STAFF USE ONLY	Type of Search					
Searcher:	NA#: AA#:					
Searcher Phone: 2-	Interference: SPDI:					
Date Searcher Picked up:	S/L: Oligomer:					
Date Completed:	Encode/Transl:					
Searcher Prep/Rev. Time:	Structure#: Text:					
Online Time:	Inventor: Litigation:					

Vendors and cost where applicable STN:
DIALOG:
QUESTEL/ORBIT:
LEXIS/NEXIS:
SEQUENCE SYSTEM:
WWW/Internet:
Other(Specify):

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AX039313 Sequence
AX039522 Sequence
AX384060 Sequence
AX3840479 Synthetic
AX039512 Sequence
AX039512 Sequence
AX039521 Sequence
AX039521 Sequence
CQ18657 Sequence
CQ186430 Sequence
CQ2348980 Sequence
CQ24888 Sequence
CQ24888 Sequence
CQ348980 Sequence
CQ348910 Sequence
CQ348910 Sequence
CQ348910 Sequence
CQ348910 Sequence
AX035914 Sequence
AX039144 Sequence
BD270481 Synthetic
AX039214 Sequence
AX039214 Sequence

Synthetic

Synthetic

ALIGNMENTS

Synthetic Sequence

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Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
Mammalia; Eutheria; Rodentia; Sciurognathi; Muridae; Murinae; Mus.
                                                                                                                                                                                                                                                                                                                                                                                           Shoshan, A., Wasserman, A., Mintz, E., Mintz, L. and Faigler, S. Oligonucleotide library for detecting rna transcripts and splice variants that populate a transcriptome Patent: WO 0210449-A 27224 07-FEB-2002;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           4058 GCAGTTTACCTCATTTGACCTTAGTTGCATGTGATCGAAATGTCTGAGTCACTGCGTGCA
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Sequence 27224 from Patent WO0210449.
CQ557589.1 GI:41524016
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Sequence 1543 from Patent WO0210449.
CQ531908
                                                                                                                                                                                                                                                                                                                                                                                                                                                          organism="Mus musculus"
/mol_type="unassigned DNA"
/db_xref="taxon:10090"
                                         AX039312
AX039521
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                                                                             AR159550
CQ080578
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Location/Qualifiers
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BD270480 Synthetic
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CQ541131 Sequence
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                                                                                                                 1 cggcacgaggaggagtggag.....gagaattcgatatcaagctt 5084
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      GenCore version 5.1.6
(c) 1993 - 2005 Compugen Ltd.
                                                                                                                                                                           Total number of hits satisfying chosen parameters:
                                                                                                                                                             4708233 segs, 24227607955 residues
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                                        nucleic search, using sw model
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Gapop 10.0 , Gapext 1.0
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Maximum Match 100%
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PAT 30-JAN-2004

linear

4117

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PAT 30-JAN-2004

linear

DNA

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Gaps ö

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Length 65; Indels

ORGANISM

VERSION KEYWORDS SOURCE

REFERENCE AUTHORS TITLE

JOURNAL

source

FEATURES

Matches

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ORIGIN

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linear PAT 18-NOV-2000
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                AGIP17/00, AGIP17/06, AGIP19/02, AGIP25/00, AGIP29/00, AGIP31/18, AGIP35/00, AGIP37/06, AGIP37/08, CO7K14/705, C12N1/15, C12N1/19, C12N1/21, PC
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synthetic construct
other sequences; artificial sequences.

I (bases I to 98)
Lawson,A.D.G. and Finney,H.M.
Synthetic transmembrane components
Agtent: UP 2002541845-A 9 10-DEC-2002;
CELITECH THERAPEUTICS LTD
OS Artificial Sequence
PD 10-DEC-2002
PP 17-APR-2000 JP 2000612453
PR 16-APR-1999 GB 9908816.3,16-APR-1999 GB 9908818.9 PI
ALASTAIR DANID GRIFFTHS LAWSON,HELENE MARGARET FINNEY PC
CIZNIS/09, AGIN38/00, AGIN48/00, AGIP1/00, AGIP3/10, AGIP3/10, AGIP3/10, PC
AGIP1/06,
PC AGIP35/00,
PC AGIP35/00, AGIP3/06, AGIP3/10, AGIP3/11, PC
PC AGIP33/06, AGIP3/06, AGIP3/10, AGIP3/11, PC
PC AGIP3/106, AGIP3/106, AGIP3/10, AGIP3/11, PC
PC AGIP3/106, AGIP3/106, AGIP3/11, PC
PC AGIP3/106, AGIP3/108, CO7K14/705, CIZNI/15, CIZNI/19, PC
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/organism='Artificial Sequence'
Location/Qualifiers
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A method of altering the properties of a membra
in by substitution of the transmembrane domain
Patent: WO 0063373-A 9 26-CCT-2000;
CELLTECH THERAPEUTICS LIMITED (GB)
LOCATION Qualifiers
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68.2%; Pred. No. 2.1e+02;
tive 0; Mismatches 27;
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/mol type="unassigned DNA"
/db_xref="taxon:32630"
/nofe="B6463"
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/mol_type="genomic DNA"
/db_xref="taxon:32630"
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Sequence 9 from Patent W00063373.
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Mammalia; Butheria; Primates; Catarrhini; Hominidae; Homo.
                                                                                                                           Eukaryota, Metazoa, Chordata, Craniata, Vertebrata, Buteleostomi,
Mammalia, Eutheria, Rodentia, Sciurognathi, Muridae, Murinae,
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          Shoshan, A., Wasserman, A., Mintz, E., Mintz, L. and Faigler, S. Oligonucleotide library for detecting rna transcripts and splice variants that populate a transcriptome patent: WO 0210449-A 10766 07-FEB-2002;
                                                                                                                                                                                                                                                Shoshan, A., Wasserman, A., Mintz, E., Mintz, L. and Faigler, S. Oligonucleotide library for detecting rna transcripts and splice variants that populate a transcriptome patent: WO 0210449-A 1543 07-FEB-2002;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  1 GAGCAGTTTACCTCATTTGACCTTAGTTGCATGTGAAATGTCTGAGTC-CTGCGTG
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88.3%; Pred. No. 4.9;
ive 0; Mismatches 7;
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/db_xref="taxon:10116"
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98.5%; Pred. No. 0.31;
tive 0; Mismatches
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                                                             Rattus norvegicus (Norway rat)
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                       GI:41498172
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SOURCE ORGANISM

AUTHORS

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Lawson, A.D. and Finney, H.M.
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                 53
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PR 16-APR-1999 GB 9908816.3,16-APR-1999 GB 9908818.9
ALASTAIR DAVID GRIFFITHS LAWSON,HELENE MARGARET FINNEY PC C12N15/09,A61K38/00,A61K48/00,A61P1/00,A61P3/10,A61P7/06, PC
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Syncheric transmembrane components
Patent: JP 2002541845-A 10 10-DEC-2002;
CELLTECH THERAPEUTICS LTD
OS Artificial Sequence
PN JP 2002541845-A/10
PD 10-DEC-2002
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Patent: WO 0063374-A 9 26-CCT-2000
CELITECH THERAPEUTICS LIMITED (GB)
LOCATION/QUALIFIERS
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AX039517
                                                             CGGGAGCTGGAGCGGCAGCGAGAGG 1528
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Matches 58; Conservative
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                      1. .100
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A method of altering the properties of a membra in by substitution of the transmembrane domain perent: WO 0063373-A 10. SC-OCT-2000; CELLIECH THERAPRUTICS LIMITED (GB)
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0.8%; Score 41.8; DB 6;
Best Local Similarity 68.2%; Pred. No. 2.1e+02;
Matches 58; Conservative 0; Mismatches 27;
Location/Qualifiers
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/organism="synthetic construct'
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Sequence 10 from Patent WO0063373
AX039309
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PAT 18-NOV-2000

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1437 AGAGCGGGAGCCCAGCAGCAGCAGCCCAAGCGGCAGCTGGAGCAGAAGCAGCTGGA 1496
                                                                                                                                                                                                                                                     Finney, H.M. and Lawson, A.D.
A method of altering the properties of a membrane-associated prote in by substitution of the transmembrane domain batent: WO 0063373-A 11 26-0CT-2000, CELLTECH THERAPEUTICS LIMITED (GB)
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0.8%; Score 40.4; DB 6;
Best Local Similarity 71.6%; Pred. No. 4.3e+02;
Matches 53; Conservative 0; Mismatches 21;
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    /note="B6465"

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Patent: WO 0063374-A 11 26-OCT-2000,
CELLTECH THERAPEUTICS LIMITED (GB)
Location/Qualifiers
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Sequence 11 from Patent WO0063373.
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ALASTAIR DAVID GRIFFITHS LAWSON,HELENE MARGARET FINNEY PC
CI2N15/09,A61K38/00,A61K48/00,A61P1/00,A61P3/10,A61P7/06, PC
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Synthetic transmembrane components
Patent: WO 0063374-A 10 26-OCT-2000;
CELLTECH THERAPEUTICS LIMITED (GB)
Location/Qualifiers
1. .100
/organism="synthetic construct"/mol_type="unassigned DNA"/db xref="taxon:32630"/note="B6464"
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Patent: JP 2002541845-A 11 10-DEC-2002;
CELLTECH THERAPEUTICS LTD
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PN JP 2002541845-A/11
PD 10-DEC-2002
PF 17-APR-2000 JP 2006612453
PR 16-APR-1999 GB 9908816.3,16-APR-15
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0; Mismatches 27;
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1 (bases 1 to 92)
Lawson, A.D.G. and Finney, H.M.
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A method of altering the properties of a membrane-associated prote in by substitution of the transmembrane domain patent: WO 0063373-A 12 26-OCT-2000;
CELLTECH THERAPEUTICS LIMITED (GB)
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PR 16-APR-1999 GB 9908818.9
ALASTAIR DAVID GRIFFITHS LAWSON HELENE WARGARET FINNEY PC
C12N15/09,A61K38/00,A61K48/00,A61P1/00,A61P3/10,A61P7/06, PC
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Location/Qualifiers
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Patent: JP 2002541845-A 12 10-DEC-2002;
CELUTECH THERAPEUTICS LTD
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Synthetic transmembrane components
Patent: WO 0063374-A 12 26-CT-2000;
CELLTECH THERAPEUTICS LIMITED (GB)
Location/Qualifiers
1. 94
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Perfect score:

1 cggcacgaggaggagtggag..........gagaattcgatatcaagctt 5084 Sequence:

IDENTITY NUC Gapop 10.0 , Gapext 1.0 Scoring table:

4390206 seqs, 2959870667 residues

4530610 Total number of hits satisfying chosen parameters:

Minimum DB seq length: 0 Maximum DB seq length: 100

Post-processing: Minimum Match 0% Maximum Match 100% Listing first 45 summaries

16Dec04:\* Genesed Database

geneseqn1980s:\*

geneseqn2003cs:\* geneseqn2003ds:\* geneseqn2002as:\*geneseqn2002bs:\* geneseqn2001bs:\* geneseqn2003as:\* geneseqn2003bs:\* geneseqn1990s:\* geneseqn2000s:\* geneseqn2001as

Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

genesegn2004as:\* genesegn2004bs:\*

	Description	Adp49483 Oligonucl	Abn54476 Mouse spl	Abn28795 Rat splic	Abn38018 Human spl	Adc16446 Short int	Adc16445 Short int	Aac65404 Oligonucl	Aac65405 Oligonucl	Abk89299 Trinucleo	Aac65406 Oligonucl	Aac65407 Oligonucl	Acd94308 Human col	Aav68382 Clone #8	Aav17232 SCA2 gene	Aav17233 SCA2 gene	Ads31430 Human gen	Aac65409 Oligonucl	Aad30431 29 mer ol	Aav17231 SCA2 gene	Aac65408 Oligonucl
SUMMARIES	. ОІ	ADP49483	ABN54476	ABN28795	ABN38018	ADC16446	ADC16445	AAC65404	AAC65405	ABK89299	AAC65406	AAC65407	ACD94308	AAV68382	AAV17232	AAV17233	ADS31430	AAC65409	AAD30431	AAV17231	AAC65408
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	* Query Match Length DB	80	65	9	9	81	81	98	100	75	92	94	97	89	78	78	69	88	87	78	98
	% Query Match	1.6	1.3	1.1	1.0	0.8	0.8	0.8	0.8	0.8	9.0	0.8	0.8	0.8	0.7	0.7	0.7	0.7	0.7	0.7	0.7
	Score	80	65	54	48.8	42.8	42.8	41.8	41.8	41	40.4	40.4	39.2	39	38	38	37.6	37	36.6	36.4	35.8
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# ALIGNMENTS

ADP49483 standard; DNA; 80 BP. RESULT 1 ADP49483

(first entry) 12-AUG-2004

ADP49483;

Oligonucleotide array related rat oligonucleotide probe No 99.

oligonucleotide array; orthologue; homology; expression distribution; change; gene-expression; rat; probe; ss.

Rattus norvegicus.

JP2004016070-A.

22-JAN-2004.

14-JUN-2002; 2002JP-00174208. 14-JUN-2002; 2002JP-00174208.

(HITA ) HITACHI LTD.

WPI; 2004-113862/12

Oligonucleotide array, useful for measuring ortholog gene-expression distribution, comprising number of oligonucleotides derived from ortholog gene of different organism immobilized on support.

Disclosure; Page 16; 56pp; Japanese.

The invention relates to a novel oligonucleotide array comprising a number of oligonucleotides derived from an orthologue gene of a different organism or species immobilised on a support body. The oligonucleotide array has two sides comprising a gene derived from two different organisms, in which one side comprises a human gene. In the oligonucleotide array a base sequence differs in a different position on the support body. Each of the oligonucleotides is a partial sequence of the orthologue gene of the organism A and organism B. The sequence match degree of the organism species A and the organism species B is less than 70%. The sequence homology of the genes other than the orthologue gene of 

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the organism species A and the organism species B is the level-of-
statistical-significance value, calculated using the homology searching
algorithm: basic local alignment search tool (BLAST) and the value is 0.1

or more. The found value or the calculated value of the melting-
temperature of the variant genes other than the orthologue gene of the

organism species A and the organism species B is 20 degrees C or more.

The oligonucleotide array is useful for measuring expression distribution
of the orthologue gene in different organisms. The method is useful for
comparing expression change of the orthologue gene with respect to
the orthologue gene in different organisms. The oligonucleotide array has
the ability to perform a measurement of gene-expression distribution of
two or more types of organism simultaneously. The oligonucleotide array in
improves reliability of measurement. This polynucleotide sequence
represents a probe of a rat gene for comparison against a human gene used
in the oligonucleotide array of the invention.
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100.0%; Pred. No. ...
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02-MAY-2001; 2001US-0287724P.
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The present invention describes oligomucleotide libraries for detecting messenger RNAs that populate a (sub-)transcriptome, where the (sub-)transcriptome comprises messenger RNAs transcribed from multiple transcription units that populate a genome. The library comprises several

Example 1; SEQ ID NO 27224; 47pp; English.

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coligonucleotides, each capable of hybridising selectively to a set of messenger RNAs transcribed from a given transcription unit of the genome, which encodes one or more messenger RNA splice variants. The coligonucleotide libraries are useful for detecting mRNAs from a biological sample, in expression profiling studies, in qualitatively or characterising the corresponding transcriptome, and in detecting RNA transcripts and splice variants of human or animal transcriptomes. The libraries may also be used as specialised mini transcriptomes. The libraries may also be used as specialised mini transcriptomes. The libraries of a sub-transcriptome under a particular biological or pathological state, and so allowing the detection of tissue or pathology-specific genes such as those genes only expressed in specific genes; and to detect RNA transcripts and splice variants of a transcriptome of a patient suffering from a particular disorder. ABN27253 to ABN59589 represent oligonucleotide sequences from trans, invention. N.B. The sequence data for this patent did not form part of the printed specification, but was obtained in electronic format
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                                                                                                                                                                                                                                                                                                                            part of the printed specification, but was obtained in electrodirectly from WIPO at ftp.wipo.int/pub/published_pct_sequences
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                                                                                                                                                                                                                                                                                                                                                                                Sequence 65 BP; 14 A; 14 C; 17 G; 20 T; 0 U; 0 Other;
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1.2e-05;
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100.0%; Pred. No. 1.2
:ive 0; Mismatches
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02-MAY-2001; 2001US-0287724P.
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nes 65; Conservative
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Example 1; SEQ ID NO 10766; 47pp; English.

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CC messenger RNAs that populate a (sub-)transcriptome, where the (sub-)transcriptome comprises messenger RNAs transcribed from multiple transcription units that populate a genome. The library comprises several oligonucleotides, each capable of hybridising selectively to a set of messenger RNAs transcribed from a given transcription unit of the genome, which encodes one or more messenger RNA splice variants. The coligonucleotide libraries are useful for detecting mRNAs from a biological sample, in expression profiling studies, in qualitatively or cannitatively characterising the corresponding transcriptom, and in detecting RNA transcripts and splice variants of human or animal conscriptomes. The libraries may also be used as specialised minical libraries to detect transcripts of a sub-transcriptome under a particular collibraries to detect transcripts of a sub-transcriptome under a particular collibraries to detect transcripts of a sub-transcriptome under a particular collogical or pathological state, and so allowing the detection of tissue condition is particular developmental specific genes; and to detect RNA transcripts and splice variants of a transcriptome of a patient suffering from a particular collogical collogical state, and so allowing from a particular collogical state, and so allowing from a particular collogical state, and so allowing from a particular collogical state, which are used in the exemplification of the printed specific particular collogical state, and so allowing from the content of the printed specification, but was obtained in electronic format and so allowing in the exemplification of the print of the coligion of the coligion o
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Sequence 65 BP; 14 A; 13 C; 18 G; 20 T; 0 U; 0 Other;

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4056 GAGCAGTTTACCTCATTTGACCTTAGTTGCATGTGATCGAAATGTCTGAGTCACTGCGTG 4115
                                                                                   1 GAGCAGTTTACCTCATTTGACCTTAGTTGCATGTGATCGAAATGTCTGAGTC-CTGCGTG 59
                               1; Gaps
 Score 54; DB 6; Length 65;
Pred. No. 0.0058;
0; Mismatches 0; Indels
1.18;
                            65; Conservative
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ABN38018 standard; DNA; 60 BP. 15-JUL-2002 ABN38018; ABN38011

ABN380 RESULT

(first entry)

Human spliced transcript detection oligonucleotide SEQ ID NO:10766.

Human, mouse, rat, splice transcript, detection, RNA transcript, splice variant; transcriptome, oligonucleotide library, ss.

Homo sapiens

WO200210449-A2.

07-FEB-2002.

20-JUL-2001; 2001WO-IB001903. 28-JUL-2000; 2000US-0221607P. 02-MAY-2001; 2001US-0287724P.

(COMP-) COMPUGEN INC

Shoshan A, Wasserman A,

New oligonucleotide libraries comprising oligonucleotides which selectively hybridize to mRNAs transcribed from a transcription unit of genome, useful for detecting tissue-, pathology-, and developmental-specific genes. WPI; 2002-257383/30.

Faigler S;

Mintz L,

Mintz E,

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The present invention describes oligonucleotide libraries for detecting messenger RNAs that populate a (sub-)transcriptome, where the (sub-)transcriptome comprises messenger RNAs transcribed from multiple transcription units that populate a genome. The library comprises several oligonucleotides, each capable of hybridising selectively to a set of messenger RNAs transcribed from a given transcription unit of the genome, which encodes one or more messenger RNA splice variants. The oligonucleotide libraries are useful for detecting mRNAs from a coligonucleotide libraries are useful for detecting mRNAs from a coligonucleotide libraries are useful for detecting mRNAs from a coligonucleotide libraries may also be used as specialised minicatering the transcripts and splice variants of human or animal transcripts and splice variants of human or animal transcripts of a sub-transcriptome under a particular biological or pathological state, and so allowing the detection of tissue and pathology-specific genes such as those genes only expressed in specific genes; and to detect RNA transcriptome of a pathent subscriptome of a pathen
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Short interfering double-stranded RNA oligonucleotide SEQ ID NO:171. expression interference; expression inhibition; target gene; short interfering double stranded RNA; cytostatic; gene therapy; proliferative disease; cancer; ds. BP ADC16446 standard; RNA; 81 (first entry) 18-DEC-2003 ADC16446; ADC16446/c THE STATE OF THE S

Synthetic.

WO2003012052-A2.

13-FEB-2003

30-JUL-2002; 2002WO-US024226. 30-JUL-2001; 2001US-0308640P. 08-APR-2002; 2002US-0370970P.

(CARN-) CARNEGIE INST WASHINGTON. (IMCO-) IMPERIAL COLLEGE INNOVATIONS LTD. (USSH ) US DEPT HEALTH & HUMAN SERVICES.

Parrish S, Mousses S; Alton EW, Griesenbach U; Morgan RA, Fire A, O, Cornelison JR, Caplen NJ, Mos Kallioniemi O,

WPI; 2003-248169/24.

New RNA comprising double stranded RNA and a 3' or 5' overhang having a length of 0-nucleotide to 5-nucleotides on each strand, useful as reverse

WPI; 2003-248169/24

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inhibition of expression of a target gene, where (1) comprises double granded RNA of 15-40 nucleotides in length and a 3 or 5 overhang having a length of 0-nucleotide to 5-nucleotides on each strand, where (1) comprises double conclectide to 5-nucleotides on each strand, where the sequence of the double stranded RNA is substantially identical to a portion of a mRNA or transcript of the target gene. Also described: (1) interfering with or inhibiting the expression of a target gene in a cell by exposing the cell to an amount of (1); (2) a gene silencing array comprising a substantially flat substrate, and addressably arrayed different double-stranded RNAs; (3) an array-based method of assessing a different double-stranded RNAs; (3) an array-based method of assessing a validating a gene as a potential drug target for a disease or condition; (5) selecting an optimised sequence of a double-stranded RNA for interference with or inhibition of expression of a target gene in a cell; and (6) a short double-stranded RNA for inhibiting expression of a target gene on a condition; inhibiting expression of a target gene on a cill; and (6) a short double-stranded RNA effective for interfering with or inhibiting expression of a target gene on a cill; inhibiting expression of a target gene comprising any of 311 20-78 nucleotide sequences (see ADC16276 to ADC16586). (1) has cytostatic
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     activity, and can be used in gene therapy. The RNAs are useful as reverse genetic and/or therapeutic tools for interfering or inhibiting expression of a target gene. They are insering for pression.
genetic and/or therapeutic tools for interfering or inhibiting expression of a target gene.
                                                                                                                                                                                              present invention describes an RNA (I) used for the interference or
                                                                                                                                   Claim 71; SEQ ID NO 171; 176pp; English.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   e.g.
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                                                                                   1445 AGCGCCAGGAGCAGGAGCCCAAGCGGCAGCTGGAGCTGGAGAAGCAGCTGGAGAAGCAGC 1504
                                                                                                              21
                                                                                                           0.8%; Score 42.8; DB 10; Length 81;
                                                        22; Indels
Sequence 81 BP; 0 A; 27 C; 27 G; 0 T; 27 U; 0 Other;
                                           3.6;
                                                        0; Mismatches
                                           Pred. No.
                                                                                                                                          1505 GGGAGCTGGAGCGGCAGC 1522
                                         71.8%;
                                                                                                                                                                      20 AGCAGCAGCAGCAGC
                                                        56; Conservative
                                           Similarity
                             Query Match
                                            Local
                                                        Matches
                                                                                                              셤
                                                                                                                                          8
                                                                                                                                                                   셤
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Short interfering double-stranded RNA oligonucleotide SEQ ID NO:170.
                                                                                                                                                                                                                                                                                        expression interference; expression inhibition; target gene; short interfering double stranded RNA; cytostatic; gene therapy;
                                                                                                                                                                                                                                                                                                                                                        proliferative disease; cancer; ds
                                                             ADC16445 standard; RNA; 81 BP
                                                                                                                                                                            (first entry)
                                                                                                                                                                               18-DEC-2003
                                                                                                                                                                                                                                                                                                                                                                                                                      Synthetic
                                                                                                                        ADC16445;
RESULT 6
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(USSH ) US DEPT HEALTH & HUMAN SERVICES. (CARN-) CARNEGIE INST WASHINGTON. (IMCO-). IMPERIAL COLLEGE INNOVATIONS LTD. 30-JUL-2002; 2002WO-US024226 30-JUL-2001; 2001US-0308640P 08-APR-2002; 2002US-0370970P WOZ003012052-A2 13-FEB-2003. 

Caplen NJ, Morgan RA, Fire A, Parrish S, Mousses S; Kallioniemi O, Cornelison JR, Alton EW, Griesenbach U;

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The present invention describes an RNA (1) used for the interference or inhibition of expression of a target gene, where (1) comprises double stranded RNA of 15-40 nucleotides in length and a 3 or 5' overhang having a length of 0-nucleotides in length and a 3' or 5' overhang continued the formal control of a manage of the double stranded RNA is substantially identical to a portion of a man or transcript of the target gene. Also described: (1) interfering with or inhibiting the expression of a target gene in a cell by exposing the cell to an amount of (1); (2) a gene silencing array comprising a substantially flat substrate, and addressably arrayed different double-stranded RNA; (3) an array-based method of assessing a phenotypic effect of a double-stranded RNA on a target gene; (4) validating a gene as a potential drug target for a disease or condition; (5) selecting an optimised sequence of a double-stranded RNA for interference with or inhibition of expression of a target gene in a cell; and (6) a short double-stranded RNA effective for interfering with or
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          ö
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               1445 AGCGCCAGGAGCAGGAGGCCAAGCGGCAGCTGGAGCTGGAGAAGCAGCTGGAGAAGCAGC 1504
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           inhibiting expression of a target gene comprising any of 311 20-78 nucleotide sequences (see ADC16276 to ADC16586). (1) has cytostatic activity, and can be used in gene therapy. The RNAs are useful as reverse genetic and/or therapeutic tools for interfering or inhibiting expression of a target gene. They are useful for treating proliferative diseases,
                                                   New RNA comprising double stranded RNA and a 3' or 5' overhang having a length of 0-nucleotide to 5-nucleotides on each strand, useful as reverse genetic and/or therapeutic tools for interfering or inhibiting expression
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       61
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 Membrane-associated protein, antiviral, antibacterial, antiparasitic, immunomodulatory, anticatory, anticatory, antialitic, antidiabetic, neuroprotective, chimeric receptor, infection, inflammatory disorder, autoimmune disorder, cancer, allergy, asthma;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          ö
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               Length 81;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      Oligonucleotide B6463 for chimeric receptor construction.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          Indels
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            cystic fibrosis; sickle cell anaemia; psoriasis; e sclerosis; organ transplant rejection; diabetes
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         Sequence 81 BP; 27 A; 27 C; 27 G; 0 T; 0 U; 0 Other;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 DB 10;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          22;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         3.6;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          0; Mismatches
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 Score 42.8;
Pred. No. 3.6
                                                                                                                                                            Claim 71; SEQ ID NO 170; 176pp; English
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  1505 GGGAGCTGGAGCGCAGC 1522
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       79
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              BP.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  17-APR-2000; 2000WO-GB001471.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    0.8%;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     71.8%;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     62 AGCAGCAGCAGCAGCAGC
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              AAC65404 standard; DNA; 98
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             14-FEB-2001 (first entry)
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          Conservative
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       transmembrane domain; ss
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    Query Match
Best Local Similarity
Matches 56; Conserv
                                                                                                                        a target gene.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       WO200063373-A1.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        e.g. cancer.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             26-OCT-2000,
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                eczema; c
multiple
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       AAC65404;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      AAC65404/c
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 셤
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       셤
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The present sequence was used in the construction of chimeric receptors.

The properties and level of expression of a membrane-associated protein may be altered by substituting a transmembrane region or a membrane-anchoring region for transmembrane or membrane-anchoring regions for transmembrane or membrane-anchoring regions that are not naturally part of the protein. The relative response of membrane-associated proteins to cell surface-associated antigen versus antigen in solution, and the sensitivity of intracellular signaling mediated by membrane-associated proteins can be altered. They can be important in treatment of, e.g. HIV infection, bacterial infections, parasitic infections, inflammatory/autoimmune disorders (e.g. rheumatoid arthritis, osteoarthritis or inflammatory bowel disease), cancer, allergic/atopic diseases (e.g. cystic fibrosis or sickle cell anaemia), dermatological disorders (e.g. cystic fibrosis or sickle cell anaemia), dermatological disorders (e.g. cygen transplant rejection, graft-versus-host diseases, or metabolic/idiopathic diseases (e.g. diabetes)
                                                                                                                                                                                                    Altering the properties or level of expression of membrane-associate proteins, e.g., to change responses to cell surface antigens or the sensitivity of intracellular signaling.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        Sequence 98 BP; 2 A; 37 C; 25 G; 34 T; 0 U; 0 Other;
                                               (CLLT ) CELLTECH THERAPEUTICS LTD.
                                                                                                                                                                                                                                                                                                       Example 2; Fig 3; 47pp; English
  99GB-00008816.
                                                                                                     Finney HM, Lawson ADG;
                                                                                                                                                  WPI; 2001-015774/02.
16-APR-1999;
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1444 GAGCGCCAGGAGCAGGAGCCAAGCGGCAGCTGGAGCTGGAGAAGCAGCTGGAGAAGCAG 1503 0; Gaps Score 41.8; DB 4; Length 98; Pred. No. 6.9; 0; Mismatches 27; Indels 1504 CGGGAGCTGGAGCGGCAGCGAGAGG 1528 CAGCAGGAGCAGCACCCAAAAG 4 68.2%; 58; Conservative Best Local Similarity Matches 58; Conserv 28 Query Match 임 ઠે ઠે g

AAC65405 standard; DNA; 100 BP (first entry) 14-FEB-2001 AAC65405; 

Oligonucleotide B6464 for chimeric receptor construction.

Membrane-associated protein; antiviral; antibacterial; antiparasitic; immunomodulatory; anticancer; antiinflammatory; antiasthmatîc; antidiabetic; neuroprotective; chimeric receptor; infection; inflammatory disorder; autoimmune disorder; cancer; allergy; asthma; eczema; cystic fibrosis; sickle cell anaemia; psoriasis; multiple sclerosis; organ transplant rejection; diabetes; transmembrane domain; ss

Synthetic

WO200063373-A1

26-OCT-2000

17-APR-2000; 2000WO-GB001471

99GB-00008816. 16-APR-1999;

(CLLT ) CELLTECH THERAPEUTICS LTD.

Finney HM, Lawson ADG;

WPI; 2001-015774/02

Altering the properties or level of expression of membrane-associated proteins, e.g., to change responses to cell surface antigens or the sensitivity of intracellular signaling.

Example 2; Fig 3; 47pp; English

The properties and level of expression of a membrane-associated procein may be altered by substituting a transmembrane region or a membrane anchoring region for transmembrane or membrane region or a membrane not naturally part of the protein. The relative response of membrane associated proteins to cell surface-associated antigen versus antigen in solution, and the sensitivity of intracellular signaling mediated by membrane-associated proteins can be altered. They can be important in treatment of, e.g. HIV infection, bacterial infections, parasitic infections, inflammatory/autoimmune disorders (e.g. rheumatoid arthritis, osteoarthritis or inflammatory bowel disease), cancer, allergic/atopic diseases (e.g. cystic fibrosis or sickle cell anaemia), dermatological disorders (e.g. cystic psoriasis), neurological disorders (e.g. wultiple sclerosis), organ transplant rejection, graft-versus-host diseases, or metabolic/idiopathic diseases (e.g. diabetes) present sequence was used in the construction of chimeric receptors

Sequence 100 BP; 34 A; 26 C; 38 G; 2 T; 0 U; 0 Other;

0; Gaps DB 4; Length 100; Score 41.8; DB 4; Length 1 Pred. No. 7; 0; Mismatches 27; Indels 0.8%; Best Local Similarity 68.2 Matches 58; Conservative Query Match

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1444 GAGCGCCAGGAGCAGGAGGCCAAGCGGCAGCTGGAGCTGGAGAAGCAGCTGGAGAAGCAG 1503 15 GAGCAGCAGGAGCAGCAGGAGCAGTAGCAGGAGCAGCAGGAGCAGCAGGAGCAGGAGCAGGAG 8 d

1504 CGGGAGCTGGAGCGCCAGCGAGAGG 1528 ଚ

75 CAGCAGGAGCAGCACCCAAAAG 99

ABK89299 standard; DNA; 75 RESULT 9 **ABK89299** 

ABK89299;

(first entry) 21-OCT-2002

Trinucleotide repeat CAG25.

Human, trinucleotide repeat instability, TNR, cancer; ds, fragile X syndrome; Huntington's disease; myotonic dystrophy; spinal and bulbar muscular atrophy; SBMA; SCA I; Kennedy's disease; spinocerebelar ataxia type I; Friedreich's ataxia; DRPLA; dentatorubaral-palidoluyalan atrophy; SCAB; SCAI2; SCA2; SCA2; SCA3; Machado-Joseph disease; testicular cancer; prostate cancer. 

Homo sapiens.

WO200257494-A1.

25-JUL-2002.

20-DEC-2001; 2001WO-US049800

21-DEC-2000; 2000US-00742025

(UYNE-) UNIV NEBRASKA.

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The invention relates to detecting (M1) alterations in trinucleotide repeat (TMR) tract lengths comprising: (i) contacting mammalian cells with a shuttle vector (containing approximately 25 repeats) that enters and replicates in the cells; (ii) recovering the replicated shuttle vector from the cells; (iii) introducing the vector into a yeast cell in the presence of a selection agent or (where the expanded TMR confers a confers resistance to the selective agent or His+ phenotype; and (iv) confers resistance to the selective agent or His+ phenotype; and (iv) celecting yeast cells with the shuttle vector containing TMR tract contextions that survived the presence of the selective agent. Also included is an adaptation of the used to detect the contraction of 33 or concern to the present invention are useful for identifying disorders with genetic alterations associated with TMR instability such as cancer especial and prostate), Fragile & Syndrome, Huntington's disease, contours and prostate), Fragile & Syndrome, Huntington's disease, contours and Kennedy's disease. The present sequence is the CAG25 TMR known contours the influent spease. The present sequence is the captod of the invantion are in the method
                                                                                                          Detecting alterations in trinucleotide repeat (TNR) tract lengths in mammalian cells useful for identifying disorders associated with TNR instability such as cancer, Fragile X syndrome, Huntington's disease or
                        Miret JJ
                                                                                                                                                                                                                                     Example 1; Page 24; 43pp; English
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              the invention for expansion
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         0.8%;
                           Pelletier R,
                                                                  WPI; 2002-575460/61
                                                                                                                                                                                         myotonic dystrophy
                        Lahue RS,
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1450 CAGGAGCAGGAGGCCCAAGCGGCAGCTGGAGAAGCAGCTGGAGAAGCAGCGGGAG 1509 . 0 Score 41; DB 6; Length 75; Pred. No. 9.5; 20; Indels Sequence 75 BP; 25 A; 25 C; 25 G; 0 T; 0 U; 0 Other; 0; Mismatches 72.68; Query Match
Best Local Similarity 72.6;
Matches 53; Conservative Н 셤 ò

1510 CTGGAGCGCCAGC 1522 CAGCAGCAGCAGC 61 ð g

AAC65406 standard; DNA; 92 BP (first entry) 14-FEB-2001 

Oligonucleotide B6465 for chimeric receptor construction.

Membrane-associated protein; antiviral; antibacterial; antiparasitic; immunomodulatory; anticancer; antiinflammatory; antiasthmatic; antidiabetic; neuroprotective; chimeric receptor; infection; inflammatory disorder; autoimmune disorder; cancer; allergy; asthma; eczema; cystic fibrosis; sickle cell anaemia; psoriasis; multiple sclerosis; organ transplant rejection; diabetes; transmembrane domain; ss

Synthetic

WO200063373-A1

26-OCT-2000.

17-APR-2000; 2000WO-GB001471.

99GB-00008816 16-APR-1999; (CLLT ) CELLTECH THERAPEUTICS LTD

Finney HM, Lawson ADG;

WPI; 2001-015774/02

expression of membrane-associated to cell surface antigens or the Altering the properties or level of exp proteins, e.g., to change responses to sensitivity of intracellular signaling.

Example 2; Fig 3; 47pp; English

The properties and level of expression of a membrane-associated protein may be altered by substituting a transmembrane region or a membrane anchoring region for transmembrane or membrane-anchoring regions that are not naturally part of the protein. The relative response of membrane-sociated proteins to cell surface-associated antigen versus antigen in solution, and the sensitivity of intracellular signaling mediated by membrane-associated proteins can be altered. They can be important in treatment of, e.g. HIV infection, bacterial infections, parasitic infections, inflammatory/autoimmune disorders (e.g. rheumator) arthritis, costeoarthritis or inflammatory bowel disease), cancer, allergic/atopic diseases (e.g. asthma or eczema), congenital disorders (e.g. cystic fibrosis or sickle cell anaemia), dermatological disorders (e.g. cystic psorialasis), neurological disorders (e.g. cygan transplant rejection, graft-versus-host diseases, or metabolic/idiopathic diseases (e.g. diabetes) construction of chimeric receptors sequence was used in the The present

Sequence 92 BP; 2 A; 34 C; 24 G; 32 T; 0 U; 0 Other;

Gaps .; 0 DB 4; Length 92; Indels 21; 0.8%; Score 40.4; DE 71.6%; Pred. No. 15; ve 0; Mismatches Local Similarity 71.6%; nes 53; Conservative Query Match Best Loca Matches

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GAAGCAGCGGGAGC 1510 GCAGGAGCAGCAGC 13 1497 ò g

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9

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AAC65407 standard; DNA; 94 RESULT 11 AAC65407

14-FEB-2001 (first entry) AAC65407;

Oligonucleotide B6466 for chimeric receptor construction.

Membrane-associated protein; antiviral; antibacterial; antiparasitic; immunomodulatory; anticancer; antiinflammatory; anticathmatic; antidiabetic; neuroprotective; chimeric receptor; infection; inflammatory disorder; autoimmune disorder; cancer; allergy; asthma; eczema; cystic fibrosis; sickle cell anaemia; psoriasis; multiple sclerosis; organ transplant rejection; diabetes; transmembrane domain; ss. 

Synthetic

WO200063373-A1.

17-APR-2000; 2000WO-GB001471

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1437 AGAGCGGGAGCGCCAGGAGCAGGAGCGAGCTGGAGCTGGAGAAGCAGCTGGA 1496
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                osteoarthritis or inflammatory bowel disease), cancer, allergic/atopic diseases (e.g. asthma or eczema), congenital disorders (e.g. cystic fibrosis or sickle cell anaemia), dermatological disorders (e.g. psoriasis), neurological disorders (e.g. multiple sclerosis), organ transplant rejection, graft-versus-host diseases, or metabolic/idiopathic diseases (e.g. diabetes)
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   The present sequence was used in the construction of chimeric receptors. The properties and level of expression of a membrane-associated protein may be altered by substituting a transmembrane region or a membrane and anchoring region for transmembrane or membrane-anchoring regions that are not naturally part of the protein. The relative response of membrane-associated proteins to cell surface-associated antigen versus antigen in solution, and the sensitivity of intracellular signaling mediated by membrane-associated proteins can be altered. They can be important in treatment of, e.g. HIV infection, bacterial infections, parasitic infections, inflammatory/autoimmune disorders (e.g. rheumacoid arthritis,
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  breast cancer; population genome analysis; genetic shift; cancer; antibiotic resistance; antibiotic non-tolerance; congenital disease; agriculture; food crop genome; resistance gene; retrovirus; influenza virus; eukaryotic pathogen detection; trypanosome; Plasmodium;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  11 AGAACAGGAGCAGCAGCAGTAGCAGGAGCAGCAGCAGGAGCAGGAGCAGGAGCA 70
                                                                                                                                                                                                                                                                                                              Altering the properties or level of expression of membrane-associated proteins, e.g., to change responses to cell surface antigens or the sensitivity of intracellular signaling.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  Gaps
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  ö
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          DB 4; Length 94;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           0; Mismatches 21; Indels
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        Sequence 94 BP; 32 A; 25 C; 35 G; 2 T; 0 U; 0 Other;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    Human colon cancer cell expressed cDNA #2720.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      Score 40.4; I
Pred. No. 15;
                                                                                                     (CLLT ) CELLTECH THERAPEUTICS LTD.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                Example 2; Fig 3; 47pp; English
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        ACD94308 standard; cDNA; 97 BP.
                                    99GB-00008816.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     99US-00406117.
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           1497 GAAGCAGCGGAGC 1510
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       1 Similarity 71.6%;
53; Conservative
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            84
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  (first entry)
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   Finney HM, Lawson ADG
                                                                                                                                                                                                                                            WPI; 2001-015774/02.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          Query Match
Best Local Similarity
Matches 53; Conserv
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  US2002155438-A1.
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         27-SEP-1999;
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    24-OCT-2002
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The invention describes a method of determining open reading frames in the genome of organism, comprising contacting mRNA from cell of organism with a single oligonucleotide primer (I) at low stringency, preparing cingle-stranded cDNA by reverse transcribing mRNA with (I), amplifying cond amplifying teps with different primers and sequencing resulting cond amplifying steps with different primers and sequencing resulting nucleotide sequence from a genome of an organism corresponds to a nucleotide sequence from a genome of an organism; and for sequencing nucleotide sequence from a genome of an organism; and for sequencing a nucleic acid molecule from a genome of an organism; and for sequencing all or part of a genome of an organism; and for sequencing all or part of a genome of an organism; and for sequencing all or part of a genome of an organism; and for sequencing all or part of a genome of an organism; and for sequencing colon cancer or breast cancer cell. The method is useful for analyses of oppulations of subjects and can be used to carry out genetic analyses of a system to determine if, e.g. there have been genetic shifts which render an individual or population more or less likely to be afflicted with congenital diseases, and the risk of affliction to a foetus, as well as through ove or sperm. The method can also be used in the study of through ove or sperm. The analyses for pathological conditions can be arried out in all animals, plants, birds, fish, etc. Using this method, and the area of agriculture, for example the genomes of food crops can be arried out in all animals, plants can be arried out in all animals, plants can be arried ont in all animals, plants can be arried ont in all animals, plants can be arried out in all animals, plants are arreaded to effect in the area of agriculture, for example the genomes of food crops can be arried ont in all animals, plants are arreaded to effect on a per more the area of agriculture, for example the genomes of food crops can be arried out in all entered to a
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        ö
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          studied to determine if resistance genes are present, defects in plant genomes can also be studied in this way. Similarly, the method permits determination of the pathogens which integrate into the genome, such as retroviruses and other integrating viruses such as influenza virus, have undergone shifts or mutations, which may require different approaches to therapy. This method is also applied to eukaryotic pathogens, such as trypanosomes, different types of Plasmodium, etc. The method essentially
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  37
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        eliminates sequencing of non-coding portions. This sequence represents a polynucleotide isolated from human colon cancer cell cDNA library
                                                                                                                                                                                                                                     Determining open reading frames of genome of an organism e.g. a human suffering from cancer involves use of single oligonucleotide primer at low stringency for preparing single-stranded cDNA from mRNA of individual.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               Gaps
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     Indels
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              Seguence 97 BP; 0 A; 39 C; 0 G; 57 T; 0 U; 1 Other;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     63.4%; Pred. No. ...,
tive 0; Mismatches 34;
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            36 AGAAGAAGAAGAAGAAGAAGAAGAAGA 4
                                                                                                                                      Brentani RR;
                                                                                                                                                                                                                                                                                                                                                                                 Example 9; Page 407; 959pp; English
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    0.8%;
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                10-MAR-1999 (first entry)
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     Matches 59; Conservative
                                                                                                                                      Simpson AJG, Neto ED,
                         (SIMP/) SIMPSON A J G. (NETO/) NETO E D.
                                                                                BREN/) BRENTANI R R.
                                                                                                                                                                                          WPI; 2003-182626/18.
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Best Local Similarity
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AAV68382/c
1D AAV6831
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CAGGAGCAGGAGGCCAAGCGGCAGCTGGAGCTGGAGCAGCTGGAGAAGCAGCGGGGAG 1509
                                                                                                                                                                                                                                                                                                                                                                                Diagnosing spinocerebellar ataxis type II - by PCR and determining number of CAG repeat units.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 This sequence represents a fragment of the SCA2 gene. It can be used in the method of the invention for diagnosing spinocerebellar ataxis type II, by performing PCR on the test DNA using two primers hybridising to parts of the SCA2 gene sequence, and determining the number of CA3 repeats in the amplified products. The method provides an easy means for the diagnosis of spinocerebellar ataxis type II
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               SCA2 gene; spinocerebellar ataxis type II; CAG repeat; PCR primer; ss.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      SCA2 gene; spinocerebellar ataxis type II; CAG repeat; PCR primer; ss.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                Sequence 78 BP; 23 A; 30 C; 25 G; 0 T; 0 U; 0 Other;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              Pred. No. 53;
0; Mismatches
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         Score 38;
Pred. No.
                                                                                                                                                                                                                                                                                                                                                                                                                                                   Disclosure; Page 13; 23pp; Japanese.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           SCA2 gene CAG repeat unit fragment.
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     BP
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                                                                                                                                                                                                                      96WO-JP001999
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         Query Match 0.7%;
Best Local Similarity 67.9%;
Matches 53; Conservative
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  CAGCAGCCGCCGCCCCGCG
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    29-JUN-1998 (first entry)
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              WPI; 1998-120796/11
                                                                                                                                                                                                                                                                                                                                            WPI; 1998-120796/11
                                                                                                                                                                                                                                                                                                       Sanpei K;
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                                                                                                                                                                                                                                                               SRLS-) SRL INC
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   (SRLS-) SRL INC
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           18-JUL-1996;
                                                                                              WO9803679-A1
                                                                                                                                                                               18-JUL-1996;
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                                                                                                                                         29-JAN-1998
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                                                         Synthetic
                                                                                                                                                                                                                                                                                                       rsuji S,
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  This sequence represents a fragment of a human CAG repeat containing clone DNA sequence isolated using the method of the invention. The method is far analysing nucleic acids in a sample, and comprises: (a) providing a sample containing nucleic acid, a first oligonucleotide primer comprising a CTG repeat, a second oligonucleotide primer comprising a CTG repeat and a polymerses and PCR reagents; (b) preparing the nucleic acid with the first and second primers; and (d) amplifying the nucleic acid with the first and second primers; and (d) attributed by the containing the amplified product. The method is used to distinguish between the expression of genes in two or more biological samples, e.g. body fluids, cells, solid tissue or solid and liquid foods. It can be used in medical disquostics, e.g. to differentiate between normal and diseased tissue or to assess the variation within monozydotic twin pairs. The method allows the isolation and analysis of genome subsets containing CAG repeats which are known to be important in a number of neurological diseases including Huntington's chorea. The method uses PCR suppression, in which only fragments which contain a target repeat are efficiently amplified. This allows accurate identification of differentially expressed genes in various cell types.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  1441 CGGGAGCCCCAGGAGCAGGAGCCCAAGCGGCAGCTGGAGCAGCAGCAGCTGGAGAAG 1500
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                                                                                                                                                                                                                                                                                                                                                                                                                                                Analysing nucleic acid samples - using amplification primers which contain CAG or CTG tri:nucleotide repeats for differential display samples from different sources.
                                                       nucleic acid analysis; variation assessment; neurological disease;
Huntington's chorea; PCR suppression; ss.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            ö
Clone #8 fragment identified by CAG repeat analysis method
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               0.8%; Score 39; DB 2; Length 89;
llarity 65.5%; Pred. No. 32;
Conservative 0; Mismatches 30; Indels
                                      repeat; human; genome analysis; medical diagnostic;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          Sequence 89 BP; 2 A; 23 C; 37 G; 27 T; 0 U; 0 Other;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    CAGCGGGAGCTGGAGCGCCAGCGAGAG 1527
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    Example, Page 32, 44pp, English.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        subsets containing CAG repeats
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hes 57; Conserv
                                                                                                                          Homo sapiens
                                                                                                                                                              WO9849345-A1
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Best Loca Matches

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RESULT 14

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0; Gaps

DB 2; Length 78; 53; 25; Indels 9

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Diagnosing spinocerebellar ataxis type II - by PCR and determining number of CAG repeat units.
                                                                                                                              This sequence represents a fragment of the SCA2 gene. It can be used in the method of the invention for diagnosing spinocerebellar ataxis type II, by performing PCR on the test DNA using two primers hybridising to parts of the SCA2 gene sequence, and determining the number of CAG repeats in the amplified products. The method provides an easy means for the diagnosis of spinocerebellar ataxis type II
                                                                                         Disclosure; Page 13-14; 23pp; Japanese.
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Score 38; DB 2; Length 78; Pred. No. 53; 0; Mismatches 25; Indels Sequence 78 BP; 23 A; 30 C; 25 G; 0 T; 0 U; 0 Other; Query Match 0.7%; Best Local Similarity 67.9%; Matches 53; Conservative

1450 CAGGAGCAGGAGGCCGAAGCTGGAGCTGGAGAAGCAGCTGGAGAAGCAGCGGGAG 1509 Gaps

; 0

1510 CTGGAGCGGCAGCGAGAG 1527

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Search completed: April 28, 2005, 08:43:20 Job time: 2467.18 secs

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BH218452 1006078G1
CD487616 Gm ckr25
AA72619 VUBB11.r
CR126087 Forward s
CG72499 OST203112
AZ476761 1M0295B19
BQ234425 hd45b08.g
CR147383 Reverse s
BQ099943 1030014C1
A1316382 uk60a03.y
CV255497 EST883874
D18610 MUSGS01671
CG724316 1119080F0
BE622032 bs11e10.y
BQ234381 hd44f06.g
A1947161 bs35g07.y
AV674805 AV674805
BQ234381 hd44f06.g

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Bay Area Functional Genomics Consortium (BayGenomics)
Email: info@baygenomics.ucsf.edu
Sequence tag generated by S. RACE of total RNA from gene trap ES
cell line. BS call lines harboring insertion mutation of target
gene are available upon request from BayGenomics. Annotation
information available from
http://baygenomics.ucsf.edu/cgi.bin/BayGearch.py?OPTION=EXACT&TYPE=
CELL_LINE&KEY=XE8464
                                                                                                                                                                                                                                                                                                                                    CC199586 94 bp mRNA linear GSS 09-MAY-2003
KE464 BayGenomics Gene Trap Library pGT1Lxf Mus musculus CDNA, mRNA
                                                                                                                                                                                                                                                                                                                                                                                                                          Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Buteleostomi;
Mammalia; Butheria; Rodentia; Sciurognathi; Muridae; Murinae; Mus.
1 (bases, 1 to 94)
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      886 CCTCCAGCAGCAGAATGGGCTGTGCCTCAGTCATCAAGGCTGAAATACAGGCAGTTATTC
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             /cell type="Embryonic stem cell"
/clone lib="BayGenomics Gene Trap Library pGT1Lxf"
/note="Vector: pGT1Lxf"
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       1.8%; Score 94; DB 8; Length 94; 100.0%; Pred. No. 2.2e-12; ive 0; Mismatches 0; Indels
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/strain="129 ola"
/db_xref="taxon:10090"
                                                                                                                                                     CG724316
BE662032
BQ234381
BQ234483
                                              CR126087
CG572499
                                                                                                                             CV295497
D18610
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BG393282
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AV674805
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Location/Qualifiers
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Unpublished (2001)
                                                                                                                                                                                                                                                                                                                                                                                                          Mus musculus (house mouse)
Mus musculus
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CC199586.1 GI:30479626
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AZ448190 IM0227
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AZ804535 ZM0065121
AZ8171347 IM0285121
AZ614077 IM0442B14
BH2255497 1006126F0
BH225549 1006126F0
CR272899 FOrward B
CR26426 Reverse 6
AZ77622 ZM0016114
AQ98931 Z6A1A04NE
CG55168 OST189766
CG340475 NISC 1204
CCA340475 NISC 1204
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                                                                              April 28, 2005, 06:48:09 ; Search time 15136.1 Seconds (without alignments) 12785.281 Million cell updates/sec
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X88324 H.sapiens D
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CO755195 Mdfrt3048
CK459729 929944 MA
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           GenCore version 5.1.6
Copyright (c) 1993 - 2005 Compugen Ltd.
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Maximum Match 100%
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gb_htc::
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GSS 29-MAY-1997

DEFINITION

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ACCESSION VERSION KEYWORDS ORGANISM

REFERENCE AUTHORS TITLE JOURNAL COMMENT

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983 GTCCCCAGGCAAGAACTATTCTCATGCAATCAAGTTTACCCCCAGGCTCAGCTGGCTTCAA 1042
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XG352 BayGenomics Gene Trap Library pGT1Lxf Mus musculus CDNA, mRNA
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Submitted (17-MAR-1995) Stylianos E. Antonarakis, Division of
Medical Genetics, University and Cantonal Hospital of Geneva, CMU,
1 rue Michel-Servet, 1211 Geneva, SWITZERLAND
Location/Qualifiers
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               Mus musculus
Eukaryota, Metazoa, Chordata, Craniata, Vertebrata, Euteleostomi,
Mammalia, Eutheria, Rodentia, Sciurognathi, Muridae, Murinae, Mus.
                                                                                                                                                                                               Bukaryota; Metazoa; Chordata; Craniata; Vertebrata; Buteleostomi; Mammalia; Butheria; Primates; Catarrhini; Hominidae; Homo.

1 (bases 1 to 64)
Chen,H., Chrast,R., Rossier,C., Morris,M.A., Lalioti,M.D. and Antonarakis,S.E.

Cloning of 559 potential exons of genes of human chromosome 21 by
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Bay Area Functional Genomics Consortium (BayGenomics)
Email: info@baygenomics.ucsf.edu
Sequence tag generated by 5' RACE of total RNA from gene trap ES
cell line. BS cell lines harboring insertion mutation of target
gene are available upon request from BayGenomics. Annotation
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                1 GTCCCCAAGCAAGAACTATTCTTATGNAGTCAAGTTTACCACAGGCTCAGNTGGNTTCAA
  HSMC18D03 64 bp DNA linear GSS 29-M
H.Bapiens DNA for trapped exon (ID HMC18D03), genomic survey
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   Chen, H.M., Rossier, C., Chrast, R. and Antonarakis, S.E. Cloning of trapped exons from human chromosome 21 Unpublished
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1.1%; Score 54.6; DB 9;
Best Local Similarity 89.1%; Pred. No. 0.021;
Matches 57; Conservative 0; Mismatches 7;
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     /organism="Homo sapiens"
/mol_type="genomic DNA"
/db_xref="taxon:9606"
/chromosome="21"
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Homo sapiens
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/dev_stage="11 weeks old"
/lab_host="SOLR (Kanamycin resistant)"
/clone_lib="Stratagene mouse skin (#937313)"
/note="Organ: skin; Vector: pBluescript SK-; Site_1:
BcoRI; Site_2: XhoI; Cloned unidirectionally. Primer:
Oligo dT: Whole skin from Il week old CS7BL/6 female mice.
Average insert size: 1.0 kb; Uni-ZAP XR Vector; ~5'
adaptor sequence: 5' CACGAGTTTTTTTTTTTTTT 3'"
                                                                                                                                                          EST 16-SEP-1997
                                                                                                                                                                                                                                                                                                                                                                                   Bukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
Mammalia; Eutheria; Rodentia; Sciurognathi; Muridae; Murinae; Mus.
1 (bases 1 to 79)
Marra,M., Hillier,L., Allen,M., Bowles,M., Dietrich,N., Dubuque,T., Geisel,S., Kucaba,T., Lacy,M., Le,M., Martin,J., Morris,M., Schellenberg,K., Steptoe,M., Tan,F., Underwood,K., Moore,B., Theising,B., Wylie,T., Lennon,G., Soares,B., Wilson,R. and
                                                                                                                                                       AA589590 179 bp mRNA linear EST 16-SEP-1997 A479099: A1 Stratagene mouse skin (#937313) Mus musculus cDNA clone IMAGE:975568 3' similar to SW:YEJ4 YEAST P4363 HYPOTHETICAL 40.4 KD PROTEIN IN PES4-HIS2 INTERGENIC REGION. ;, mRNA sequence.
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        Contact: Marra Mimouse EST Project
Washl-HMI Mouse EST Project
Washlington University School of MedicineP
4444 Forest Park Parkway, Box 8501, St. Louis, MO 63108
Tel: 314 286 1810
Fax: 314 286 1810
Email: mouseest@watson.wustl.edu
This clone is available royalty-free through LLNL; contact the
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            1 TGCCATGTACACATACGAGAGTTCTGATCAAGGAGATTTAAAGTTTCAGCAAGGGGATGT
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Seq primer: -20ml3 rev1 ET from Amersham
High quality sequence stop: 1.
Location/Qualifiers
61 AACAGCCACGACAAAACTATGAGTGGACACTTAA 94
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/clone="IMAGE:975568"
/sex="females"
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/strain="C57BL/6"
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Mus musculus
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FEATURES

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/sex="Male"
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KEYWORDS
SOURCE
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                         http://baygenomics.ucsf.edu/cgi-bin/BaySearch.py?OPTION=EXACT&TYPE=
CELL_LINE&KEY=XG352
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was hydrodynamically sheared by repeated passage through a
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1 (ba
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              AZ786638 92 bp DNA linear GSS 16-FEB-200
2M0032E18F Mouse 10kb plasmid UUGC1M library Mus musculus genomic
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 Contact: Robert B. Weiss
University of Utah Genome Center
University of Utah
University of Utah
Rm. 308, Biomedical Polymers Research Bldg., 20 S. 2030 E., SLC,
84112, USA
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                                                                                                                                                                                                                                                                                                                                                                              /cell_type="Embryonic stem cell"
/clone_lib="BayGenomics Gene Trap Library pGT1Lxf"
/note="Vector: pGT1Lxf"
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Insert Length: 10000 Std Error: 0.00
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Seg primer: CGTTGTAAAACGACGCCCAGT
Class: plasmid ends
                                                                                                                                                                                                              organism="Mus musculus"
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/strain="C57BL/6J"
                                                                                                                                                                                                                                                                                                                /db_xref="taxon:10090"
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/clone="UUGC2M0032E18"
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Location/Qualifiers
                                                                                                     Class: Gene Trap.
Location/Qualifiers
                                                                                                                                                                                                                                        /mol_type="mRNA"
/strain="129 ola"
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Plate: 0032 row: R ~
information available
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Fax: 801 585 7177
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AZ786638/c
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ORGANISM
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0.005 inch orifice at constant velocity. The sheared DNA was blunt end-repaired with T4 DNA polymerase and T4 polymuclectide kinase. Adaptor oligonuclectides were ligated to the blunt ends in high molar excess. The adaptored DNA was purified and size selected for a 9.5 to 10.5 kb range using preparative agarose gel electrophoresis. Vector DNA was prepared from a derivative of pWD42 (gil4732114|gb|AR12972.1), a copy-number inducible derivative of plasmid R1. The vector was ligated with adaptors complementary to the insert adaptors and purified. The sheared, adaptored mouse DNA was annealed to adaptored vector DNA, and transformed into chemically-competent B. coli Xi10-GG1d (Stratagene) cells and selected for ampicillin resistance."
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Dunn,D., Aoyaqi,A., Barber,M., Beacorn,T., Duval,B., Hamil,C., Islam,H., Longacre,S., Mahmoud,M., Meenen,E., Pedersen,T., Nese,M., Rose,R., Stokes,R., Tingey,A., von Niederhausern,A. and Wright,D., Weise,R.
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/note="Vector: PWD42nv; Purified genomic DNA from M.
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0.9%; Score 44; DB 8; Length 92;
Best Local Similarity 67.4%; Pred. No. 12;
Matches 62; Conservative 0; Mismatches 30; Indels
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University of Utah Genome Center
University of Utah
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/strain="C57BL/6J"
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/clone="UUGC1M0245A17"
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Fax: 801 585 7177
Email: ddunn@genetics.utah.edu
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Location/Qualifiers
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69.6%; Pred. No. 86; tive 0; Mismatches
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                      55; Conservative
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Fax: 801 585 7177
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Rm. 308, Bio
USA
  Best Local Similarity
                           Matches
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AUTHORS
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AZ804535
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KEYWORDS
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                                       (http://www.jax.org/resources/documents/dnares/). The DNA was hydrodynamically sheared by repeated passage through a 0.005 inch orifice at constant velocity. The sheared DNA was blunt end-repaired with T4 DNA polymerase and T4 polymucleotide kinase. Adaptor oligonucleotides were ligated to the blunt ends in high molar excess. The adaptored DNA was purified and size-selected for a 9.5 to 10.5 kb range using preparative agarose gelectrophoresis. Vector DNA was prepared from a derivative of pwAPA2 (gel 4732114|gb|AR129072.1), a copy-number inducible derivative of plasmid R1. The vector was ligated with adaptors complementary to the insert adaptors and purified. The sheared, adaptored mouse DNA was annealed to adaptored vector DNA, and transformed into chemically-competent E. coli XII.0-Gold (Stratagene) cells and selected for ampicillin resistance."
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AV533640.1 GI:8693923
EST.
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DNA Res. 7 (3), 175-180 (2000)
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Email: asamizu@kazusa.or.jp, URL:http://www.kazusa.or.jp/en/plant/.
Location/Qualifiers
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/tissue type="flower buds"
/clone lib="Arabidopsis thaliana flower buds Columbia"
/note="Vector: pBluescriptII SK-; Site_I: EcoRI; Site_2:
XhoI"
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    musculus C57BL/6J (male) was obtained from the Jackson
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 0; Gaps
                                                                                                                                                                                                                                                                                                                                                                                                                                                                              0.8%; Score 42.8; DB 8; Length 89; 68.6%; Pred. No. 24; ive 0; Mismatches 27; Indels
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Kazusa DNA Research Institute
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         organism="Arabidopsis thaliana"
                             Laboratory Mouse DNA Resource
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Arabidopsis thaliana
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               /mol_type="mRNA"
/ecotype="Columbia"
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          Contact: Erika Asamizu
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   Query Match
Best Local Similarity 68.6
Matches 59; Conservative
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              VERSION
KEYWORDS
SOURCE
ORGANISM
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TITLE
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MEDLINE
PUBMED
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g ò

8

DB 1; Length 86;

0.8%; Score 40.6;

Query Match

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/lab host="E. Coli strain XL10-Gold, T1-resistant, F-"
/clone lib="Mouse 10kb plasmid UUGCLM library"
/clone lib="Wouse 10kb plasmid UUGCLM library"
/note="Vector: PWD42nv; Purified genomic DNA from M.
musculus C57BL/6J (male) was obtained from the Jackson
Laboratory Mouse DNA Resources/documents/Inares/). The DNA
was hydrodynamically sheared by repeated passage through a
0.005 inch orifice at constant velocity. The sheared DNA
was hydrodynamically sheared by repeated passage through a
0.005 inch orifice at constant velocity. The sheared DNA
was hydrodynamically sheared by respected for a polynuclectide kinase. Adaptor oligonuclectides were
ligated to the blunt ends in high molar excess. The
adaptored DNA was purified and size-selected for a 9.5 to
10.5 kb range using preparative agarose gel
electrophoresis. Vector DNA was prepared from a derivative
of pWD42 (gil 4732114 [gb]AP129072.1), a copy-number
inducible derivative of plasmid R1. The vector was ligated
with adaptors complementary to the insert adaptors and
purified. The sheared, adaptored mouse DNA was annealed to
adaptored vector DNA, and transformed into
chemically-competent E. coli XL10-Gold (Stratagene) cells
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                                                               1458 GGAGGCCAAGCGGGCAGCTGGAGAAGCAGCTGGAGAAGCAGCGGGGGGGCTGGAGCC
                                                                                                                                                                                                                                                                                                                                                                                                                                                                  AZ804535
2M0065121R Mouse 10kb plasmid UUGC1M library Mus musculus genomic clone UUGC2M0065121 R, genomic survey sequence.
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Dunn, D., Aoyagi,A., Barber,M., Bacorn,T., Duval,B., Hamil,C., Islam,H., Longarers,S., Mammoud,M., Meenen,E., Pedersen,T., Reilly,M., Rose,M., Rose,R., Stokes,R., Tingey,A., von Niederhausern,A. and Wright,D.,Weiss,R.
Mouse whole genome scaffolding with paired end reads from 10kb plasmid inserts
Unpublished (2000)
                                                                                                                                           20
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   Indels
   24;
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Insert Length: 10000 Std Error: 0.00
Plate: 0065 row: I column: 21
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     Plate: 0065 row: I column: 21
Seg primer: CACACAGGAAACAGCTATGACC
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/mol type="genomic DNA"
/strain="C57BL/6J"
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          Contact: Robert B. Weiss
University of Utah Genome Center
University of Utah
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/clone="UUGC2M0065I21"
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Location/Qualifiers
                                                                                                                                                                                                                         1518 GCAGCGAGAGGAGGAGGG 1536
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     Mus musculus (house mouse)
Mus musculus
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RESULT 9

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Best Local Similarity
Matches 49; Conserv
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84112, USA
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   GSS
                                                                                                                                                                         Query Match
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AZ837486/c
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          SOURCE
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                                                                                                                                                                                                                                                                                                                                                                                                                                      AZ471347 1000 100 DNA linear GSS 04-OCT-2000 1M0285I21R Mouse 10kb plasmid UUGCIM library Mus musculus genomic clone UUGCIM0285I21 R, genomic survey sequence.
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                                                                                                                                                                    1457 AGGAGGCCAAGCGGCAGCTGGAGCAGCAGCTGGAGAAGCAGCAGCGGGAGCTGGAGC 1516
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Wakaryota, Metazoa; Chordata; Craniata; Vertebrata; Buteleostomi;
Mammalia; Butheria; Rodentia; Sciurognathi; Muridae; Murinae; Mus
1 (bases 1 to 71)
                                                                                                                                                                                                                    61
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           plasmid inserts
Unpublished (2000)
Contact: Robert B. Weiss
University of Utah Genome Center
University of Utah
Rm. 308, Biomedical Polymers Research Bldg., 20 S. 2030 E., SLC,
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   /lab_host="E. Coli strain XL10-Gold, T1-resistant, F-"
/clone_lib="Mouse_10kb plasmid UTGCIM library"
/note="Vector: PWD42lv; Purified genomic DNA from M.
musculus C57BL/6J (male) was obtained from the Jackson
                                                                                                                                                                                                                    Dunn, D., Aoyagi, A., Barber, M., Beacorn, T., Duval, B., Hamil, C., Islam, H., Longacre, S., Mahmoud, M., Meenen, E., Pedersen, T., Reilly, M., Rose, M., Rose, R., Stokes, R., Tingey, A., von Niederhausern, A. and Wright, D., Weiss, R.
                                                                                                                       Gaps
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                                                                         Length 94;
                                                                                                                    31; Indels
and selected for ampicillin resistance."
                                                                         DB 8;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       Email: ddunn@genetics.utah.edu
Insert Length: 10000 Std Error: 0.00
Plate: 0285 row: I column: 21
Seg primer: CACACAGGAAACAGCTATGACC
Class: plasmid ends
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     Laboratory Mouse DNA Resource
                                                                                                                                                                                                                                                               1517 GGCAGCGAGAGGAGGAGGAGGAGA 1546
                                                                      Query Match

0.8%; Score 40.4; D

Best Local Similarity 65.6%; Pred. No. 99;
Matches 59; Conservative 0; Mismatches
                                                                                                                                                                                                                                                                                              62 AGGAGGAGGAGGAGGAGGAGGAGAG 91
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              /mol_type="genomic DNA"
/strain="C57BL/6J"
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              /db_xref="taxon:10090"
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Location/Qualifiers
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       Mus musculus (house mouse)
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         Tel: 801 585 5606
Fax: 801 585 7177
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KEYWORDS
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TITLE

COMMENT

FEATURES

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/lab host="B. Coli strain XL10-Gold, T1-resistant, F-"
/lab host="B. Coli strain XL10-Gold, T1-resistant, F-"
/clone lib="Wouse 10kb plasmid UUGCIM library"
/note="Vector: PWD42nv; Purified genomic DNA from M.
musculus C57BL/6J (male) was obtained from the Jackson
Laboratory Mouse DNA Resources/documents/dnares/). The DNA
was hydrodynamically sheared by repeated passage through a
0.005 inch orifice at constant velocity. The sheared DNA
was blunt end-repaired with T4 DNA polymerase and T4
polynucleotide kinase. Adaptor oligonucleotides were
ligated to the blunt ends in high molar excess. The
adaptored DNA was purified and size-selected for a 9.5 to
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Bukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;

Bukaryota; Metazoa; Rodentia; Sciurognathi; Muridae; Murinae; Mus.

Dann,D., Aoyagi,A., Barber,M., Beacorn,T., Duval,B., Hamil,C.,

Islam,H., Longacre,S., Mahmoud,M., Meenen,B., Pedersen,T.,

Reilly,M., Rose,M., Rose,R., Stokes,R., Tingey,A., von

Niederhausern,A. and Wright,D.,Weiss,R.,

Mouse whole genome scaffolding with paired end reads from 10kb

plasmid inserts

Unpublished (2000)

Contact: Robert B. Weiss

University of Utah Genome Center

University of Utah Genome Center

University of Utah Canome Center

University of Utah Canome Center
with adaptors complementary to the insert adaptors and purified. The sheared, adaptored mouse DNA was annealed to adaptored vector DNA, and transformed into chemically-competent E. coli Xil0-Gold (Stratagene) cells and selected for ampicillin resistance."
                                                                                                                                                                                                                                                                                                                                                                                                1477 GAGCTGGAGAAGCAGCTGGAGAAGCAGCGGGAGCTGGAGCGGCAGCGAGGAGGAGGAGGAGG
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2M0132J14R Mouse 10kb plasmid UUGC1M library Mus musculus genomic clone UUGC2M0132J14 R, genomic survey sequence.
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0
                                                                                                                                                                                                                                                0.7%; Score 36.4; DB 8; Length 71;
ilarity 70.0%; Pred. No. 9.5e+02;
Conservative 0; Mismatches 21; Indels
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Insert Length: 10000 Std Error: 0.00
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Seg primer: CACACAGGAAACAGCTATGACC
Class: plasmid ends
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/organism="Mus musculus"
/mol_type="genomic DNA"
/strain="C57BL/6J"
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   /db_xref="taxon:10090"
/clone="UUGC2M0132J14"
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Location/Qualifiers
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Fax: 801 585 7177
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DRIGIN

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Laboratory Mouse DNA Resource (http://www.jax.org/resources/documents/dnares/). The DNA was hydrodynamically sheared by repeated passage through a was hydrodynamically sheared by repeated passage through a onos inch orifice at constant velocity. The sheared DNA
10.5 kb range using preparative agarose gel electrophoresis. Vector DNA was prepared from a derivative of pMO42 [gi|4732114[gb|AR129072.1], a copy-number inducible derivative of plasmid R1. The vector was ligated with adaptors complementary to the insert adaptors and purified. The sheared, adaptored mouse DNA was annealed to adaptored vector DNA, and transformed into adaptorebent E. coli X11.0-Gold (Stratagene) cells and selected for ampicillin resistance."
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Eukaryota, Metazoa, Chordata, Craniata, Vertebrata, Euteleostomi,

Bukaryota, Metazoa, Chordata, Craniata, Muridae, Muridae, Musilae, Eutheria, Rodentia, Sciurognathi, Muridae, Musila, 1 (Dases 1 to 91)

Bunn, D., Aoyagi, A., Barber, M., Beacorn, T., Duval, B., Hamil, C.,

Ballam, H., Longacre, S., Mahmoud, M., Meenen, E., Pedersen, T.,

Reilly, M., Rose, M., Rose, M., Stokes, R., Tingey, A., von

Niederhausern, A. and Wright, D., Weiss, R.

Mouse whole genome scaffolding with paired end reads from 10kb
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1M0442B14R Mouse 10kb plasmid UUGCIM library Mus musculus genomic clone UUGCIM0442B14 R, genomic survey sequence.
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Unpublished (2000)
Context: Robert B. Weiss
University of Utah Genome Center
University of Utah
Rm. 308, Biomedical Polymers Research Bldg., 20 S. 2030 E., SLC,
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                                                                                                                                                                                                                                                                                                  ch 0.7%; Score 36.2; DB 8; Length 87; 1 Similarity 68.5%; Pred. No. 1.1e+03; 50; Conservative 0; Mismatches 23; Indels
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Insert Length: 10000 Std Error: 0.00
Plate: O442 row: B column: 14
Seg primer: CACACAGGAAACAGCTATGACC
Class: plasmid ends
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/mol_type="genomic DNA"
/strain="C57BL/6J"
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  High quality sequence stop: 91.
Location/Qualifiers
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clone="UUGC1M0442B14"
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               Mus musculus (house mouse)
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              AZ614077.1 GI:11736267
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            sex="Male"
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     1530 GGAGAGGAGGAAG 1542
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          26 GAAAAGGAGAAGG 14
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     Tel: 801 585 5606
Fax: 801 585 7177
                                                                                                                                                                                                                                                                                                           Query Match
Best Local Similarity
Matches 50; Conserv
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 USA
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AZ614077/c
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ORGANISM
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KEYWORDS
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TITLE

COMMENT

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/tissue type="ladult"
/dev_stage="adult"
/dev_stage
was blunt end-repaired with T4 DNA polymerase and T4 polymucleotide kinase. Adaptor oligonucleotides were ligated to the blunt ends in high molar excess. The adaptored DNA was purified and size-selected for a 9.5 to 10.5 kb range using preparative agarose gel electrophoresis. Vector DNA was prepared from a derivative of pwD42 (gi|4732114|gb|AF129072.1), a copy-number inducible derivative of plasmid R1. The vector was ligated with adaptors complementary to the insert adaptors and purified. The sheared, adaptored mouse DNA was annealed to
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                GSS 08-NOV-2001
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Unpublished (2001)
Contact: Walbot V
                                                                                                                                                                                                                                                                                                                                                                                                                        adaptored vector DNA, and transformed into chemically competent E. coli XL10-Gold (Stratagene) cells and selected for ampicillin resistance."
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        Eukaryota, Viridiplantae; Streptophyta; Embryophyta; Tracheophyta; Spermarophyta; Magnoliophyta; Liliopsida; Poales; Poaceae; PACCAD clade; Panicoideae; Andropogoneae; Zea.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  23
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              755. California Ave, Palo Alto, CA 94304, USA
141: 650 723 2221
Fax: 650 725 8221
Fax: 150 725 8221
Possible ligation site so sequence was trimmed. Post-ligation sequence submitted separately.
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/cul_tivar="mixed background W23/A188/B73"
/db_xref="taxon:4577"
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0.7%; Score 36.2; DB 8;
Best Local Similarity 65.4%; Pred. No. 1.2e+03;
Matches 53; Conservative 0; Mismatches 28;
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BH225497/c
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1374 GGAGCAGCAGCGCAAAGAGCAGGAGCGGTTGGCTCAGCTGGAGCGCGCCCGAGCAGGAGAG 1433
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    (Dases 1 to 91)

                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 genomic sequences found using engineered RescueMu transposon
                                                                                                                    85 GGAGGAGACGCCCAAGGAACAGGAGCGTAAGGAGGAGGAGGAGGTGGAGGCGGGGGAGAG 26
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1006126H07.x1 1006 - RescueMu Grid G Zea mays genomic, genomic
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Possible ligation site so sequence was trimmed. Post-ligation
sequence submitted separately.
Plate: 1006126 row: 1
Class: transposon.tagged.
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/cultivar="mixed background W23/A188/B73"
/db_xref="taxon:4577"
         Pred. No. 1.3e+03;
0; Mismatches 30; Indels
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Tel: 650 723 2227
Fax: 650 725 8221
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Contact: Walbot V
Department of Biological Sciences
                                                                                                                                                                 1434 GAAAGAGCGGGAGCGCCAGGAGCA 1457
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/organism="Zea mays"
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                                                                                                                                                                                                        25 GAAGACCCAGGAGCCGCCGCAGCA
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         64.38;
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                              54; Conservative
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BH225549
         Best Local Similarity
Matches 54; Conserv
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les 54; Conserv
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BH225549/c
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KEYWORDS
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/tissue_type="leaf".
/dow_stage="leaf".
/dow_host="Noof" - RescueMu Grid G"
/clone lib="loof" - RescueMu Grid G"
/clone lib="loof" - RescueMu Grid G"
/clone lib="loof" - Site l: BamHi, Site 2: BgJII;
RescueMu is a 4.9 bb, modified maize Mu transposon
designed to allow plasmid rescue from total genomic DNA.
Mu elements insert preferentially into transcription
units. For more information on RescueMu, go to the web
site 'www.zamdb.iastate.edu' and follow the links for
'RescueMu.' Grid G was grown at Stanford in 2000. DNA was
extracted from leaf punches, double digested using BamHi
and BgJII, and ligated to form circular plasmids. DH10B
cells were transformed and then screened on LB plates with
'RescueMu.' Grid G was grown at Stanford in 2000. DNA was extracted from leaf punches, double digested using BamHI and B9111, and ligated to form circular plasmids. DH10B cells were transformed and then screened on LB plates with
                                                                                                                                                                                                                                                     1374 GGAGCAGCACACACAAAAAGAGCAGGAGCGGTTGGCTTCAGCTGGAGCGCCGCCGAGCAGGAGAG 1433
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 08-NOV-2001
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Unpublished (2001)
Contact: Walbot V
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    (bases 1 to 91)

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                                                                                                                                                                                                                                                                                                  85 GGAGGAGACGCCAAGGAACAGGAGCGTAAGGAGGAGGAGGAGGAGGAGGAGGAGAGA
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1006126604.x1 1006 - RescueMu Grid G Zea mays genomic, genomic
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                                                                                                                                                                 Length 91;
                                                                                                                                                             Score 36; DB 8; Length 91;
Pred. No. 1.3e+03;
0; Mismatches 30; Indels
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Mol_type="genomic DNA"
(cultivar="mixed background W23/A188/B73"
/db_xref="taxon:4577"
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B155 California Ave, Palo Alto, CA 94304, USA
Tel: 650 723 7227
Fax: 650 725 8221
Email: walbot@stanford.edu
Possible ligation site so sequence was trimm
sequence submitted separately.
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                                                                                                                                                                                                                                                                                                                                                                                          GAAGACCCAGGAGCCGCCGCAGCA 2
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Location/Qualifiers
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          survey sequence.
BH225515
BH225515.1 GI:16823551
                                                                                                                                                             0.7%;
Similarity 64.3%;
54; Conservative (
                                                                                               ampicillin."
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                                                                                                                                                             Query Match
Best Local S
Matches 54
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BH225515/c
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SOURCE
ORGANISM
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VERSION
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TITLE
JOURNAL
COMMENT
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                                                                                                                                            Length 91;
                                                                                                                                                           30;
                                                                                                                                          0.7%; Score 36; DB 8; I
llarity 64.3%; Pred. No. 1.3e+03;
Conservative 0; Mismatches 30;
                                                                                                                                                                                                            1434 GAAAGAGCGGGAGCGCCAGGAGCA 1457
/dev_stage="adult"
/lab_host="DH108"
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0.7%; Score 36; DB 8; Length 91;

Query Match

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RESULT 15
CR272899/C
LOCUS
DEFINITION
CR272899
CR27289
CR27280
CR
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35 AAGAGGAAĞAGGAAĞAGGAAĞAĞĞ 6

1525 GAGGAGGAGGAGGAAGGAGTCGAGAGG 1554

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Search completed: April 29, 2005, 02:01:57 Job time: 15142.1 secs

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Sequence 4823, Ap
Sequence 20105, A
Sequence 24, Appl
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                                                                      April 28, 2005, 07:02:07 ; Search time 760.328 Seconds (without alignments) 10941.112 Million cell updates/sec
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Appli
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                                                                                                                                                                                                                                                                                                                                                                                                                                                     Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.
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.: /cgn2_6/ptodata/1/ina/5B_COMB.seq:*

.: /cgn2_6/ptodata/1/ina/6A_COMB.seq:*

.: /cgn2_6/ptodata/1/ina/PCTUS_COMB.seq:*

.: /cgn2_6/ptodata/1/ina/PCTUS_COMB.seq:*
GenCore version 5.1.6
Copyright (c) 1993 - 2005 Compugen Ltd.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    US-09-043-303-12
US-09-573-080A-463
US-09-043-303-11
US-09-043-303-11
US-09-043-303-13
US-09-043-303-13
US-09-573-080A-462
US-09-573-080A-462
US-09-573-080A-462
US-09-573-080A-462
US-08-56-978B-24
US-08-56-978B-24
US-08-56-978B-24
US-08-18-220-26
US-07-812-421-26
US-07-812-421-26
US-07-812-421-25
US-08-823-771-57
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S-09-281-481A-7
S-09-513-999C-35527
S-09-513-999C-29269
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US-08-860-038-15
                                                                                                                                                                                                               1202784 seqs, 818138359 residues
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Maximum Match 100%
Listing first 45 summaries
                                                nucleic search, using sw model
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5084
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Match Length
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Maximum DB seq length: 100
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31.4
30.4
30.4
30.2
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28.4
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Perfect score:
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Sequence 463, Application US/09573080A

Sequent No. 6828097

GREEAL INFORMATION:
GREEAL INFORMATION:
APPLICANT: JOAN, KNOLL
APPLICANT: ROGAN, PETER
TITLE OF INVENTION: SINGLE COPY GENOMIC HYBRIDIZATION PROBES AND METHOD OF GENERATING THE REPERBENCE: 3030, 800A
CURRENT FILING DATE: 2000-05-16
NUMBER OF SEQ ID NOS: 479
SOFTWARE: Patentin version 3.0
SEQ ID NO 463
LENGTH: 69
                                                                                                                                                                                                                                                                                                                            Sequence 12, Application US/09043303

Patent No. 6251589

GENERAL INFORMATION:

APPLICANT: TSUJI, Shaji

TITLE OF INVENTION: Finers Therefor

TITLE OF INVENTION: Piners Therefor

FILE REFRENCE: 0760-0241P

CURRENT APPLICATION NUMBER: US/09/043,303

CURRENT APPLICATION NUMBER: PCT/JP96/01999

EARLIER APPLICATION NUMBER: PCT/JP96/01999

SARLIER PILING DATE: 1996-07-18

NUMBER OF SEQ ID NOS: 17

SOFTWARE: PATENTI Ver. 2.0

LENGTH: 78
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                                                                                       US-08-477-509B-58
US-08-707-237A-29
US-08-482-085B-58
US-08-475-411A-25
US-08-478-029A-25
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US-09-573-080A-468
                                                    PCT-US92-06412-88
                                                                                                                                                                                    US-08-182-175A-89
US-08-474-633A-66
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                                                               US-07-609-716-25
US-08-175-155-23
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                                                                                                                                                                                                                JS-08-823-771-66
                                                                                                                                                                                                                                                                   ALIGNMENTS
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il Similarity 67.9%;
53; Conservative
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ORGANISM: Homo sapiens
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Best Local Similarity
Matches 53; Conserv
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US-09-573-080A-463
                                                                                                                                                                                                                                                                                                                       US-09-043-303-12
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28.5.5.5
28.5.5.5
28.5.5.5
28.5.5
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Gaps ;

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Query Match 0.7%; Score 34; DB 3; Length 75; Best Local Similarity 66.2%; Pred. No. 47; Matches 49; Conservative 0; Mismatches 25; Indels
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APPLICANT: ROGAN, PETER
TITLE OF INVENTION: SID
FILE REFERENCE: 30307
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   NUMBER OF SEQ ID NOS: 17
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           TYPE: DNA ORGANISM: Homo sapiens
LENGTH: 75
TYPE: DNA
ORGANISM: Homo sapiens
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SOFTWARE: Pat
SEQ ID NO 13
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                                                             CTHER INFORMATION: Description of Artificial Sequence: repetitive sequence found in CTHER INFORMATION: many eutherial genomes. Length of core repeating element is vari; OTHER INFORMATION: able and is often polymorphi US-09-573-080A-463
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| Sequence 10, Application US/09043303
| Patent No. 6251589
| GENERAL INFORMATION:
| APPLICANT: TSUJI: Shoji
| APPLICANT: SAUPEI, Kazujiro
| TITLE OF INVENTION: Method for Diagnosing Spinocerebellar Alaxia Type 2 and TITLE OF INVENTION: Pitners Therefor
| TITLE OF INVENTION: Pitners Therefor
| FILE REFERENCE: 0760-0241P
| CURRENT APPLICATION NUMBER: US/09/043,303
| CURRENT FILING DATE: 1998-05-18
| EARLIER FILING DATE: 1996-07-18
| NUMBER OF SEQ ID NOS: 17
| SOFTWARE: Patentin Ver. 2.0
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APPLICANT: TSUJISON:
APPLICANT: TSUJISON:
APPLICANT: TSUJISON:
APPLICANT: TSUJISON:
APPLICANT: TSUJISON:
TITLE OF INVENTION: Primers Therefor
TITLE OF INVENTION: Primers Therefor
FILE REPREMENTE: 076-02419
CURRENT APPLICATION NUMBER: US/09/043,303
CURRENT FILING DATE: 1998-05-18
EARLIER APPLICATION NUMBER: PCT/JP96/01999
EARLIER FILING DATE: 1966-07-18
NUMBER OF SEQ ID NOS: 17
SOFTWARE: Patentin Ver. 2.0
SEQ ID NO 11
LENGTH: 78
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Pred. No. 5;
0; Mismatches 19; Indels
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66.7%; Pred. No. 11;
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US-09-043-303-11
Sequence 11, Application US/09043303
; Patent No. 6251589
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Best Local Similarity 72.1%;
Matches 49; Conservative
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Best Local Similarity 66.7
Matches 52; Conservative
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                                                                                                                                                                                                                                                                                                                                                                                                                        61 GCAGCAGC 68
                                   ORGANISM: Artificial FEATURE:
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SINGLE COPY GENOMIC HYBRIDIZATION PROBES AND METHOD OF GENERATIN
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1454 AGCAGGAGGCCAAGCGGCAGCTGGAGCTGGAGAAGCAGCTGGAGAAGCAGCGGGAGCTGG 1513
                                                                                                                                                                                                                                                                                          US-09-043-303-13

Sequence 13, Application US/09043303

Sequence 13, Application US/09043303

Sequence 13, Application US/09043303

GENERAL INFORMATION:

APPLICANT: TSUJI, Shoji

APPLICANT: SANPEI, Kazujiro

TITLE OF INVENTION: Primers Therefor

TITLE OF INVENTION: Primers Therefor

FILE REFERENCE: 0760-0241P

CURRENT APPLICATION NUMBER: US/09/043,303

CURRENT PILING DATE: 1998-05-18

EARLIER FILING DATE: 1998-05-18

EARLIER PILING DATE: 1996-07-18
                                                      1466 AGCGGCAGCTGGAGCAGCAGCTGGAGAAGCAGCGGGAGCTGGAGCGGGCAGC 1522
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 DB 4; Length 69;
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  US-09-573-080A-462;
Sequence 462, Application US/09573080A;
Patent No. 6828097;
GRNERAL INFORMATION:
                                                                                                                           1514 AGCGGCAGCGAGAG 1527
                                                                                                                                                                              62 AGCCGCCGCCGCG 75
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    PatentIn Ver. 2.0
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Best Local Similarity 73.7
Matches 42; Conservative
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RESULT 9
US-08-556-978B-24
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                                                                  1467 GCGGCAGCTGGAGCTGGAGAAACAGCTGGAGAAGCAGCGGGAGCTGGAGCGGCAGCAGAAA 1526
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                                                                                                                                                                                                                                                                                     Sequence 4823, Application US/09270767

Fatent No. 6703491

GENERAL INFORMATION:
APPLICANT: Homburset al.
TITLE OF INVENTION: Nucleic acids and proteins of Drosophila melanogaster
FILE REFERENCE: File Reference: 7326-094

CURRENT APPLICATION NUMBER: US/09/270,767

CURRENT FILING DATE: 1999-03-17

NUMBER OF SEQ ID NOS: 62517

SOFTWARE: PatentIn Ver. 2.0
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      GENERAL INFORMATION:
APPLICANT: Homburger et al.
APPLICANT: Homburger et al.
TITLE NEW INVENTION: Nuclei acids and proteins of Drosophila melanogaster
FILE REFERENCE: File Reference: 7326-094
CURRENT APPLICATION NUMBER: US/09/270,767
CURRENT FILING DATE: 1999-03-17
NUMBER OF SEQ ID NOS: 62217
SOFTWARE: Patentin Ver. 2.0
SEQ ID NO 20105
LENGTH: 89
                                                                                            Gaps
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Pred. No. 2.6e+02;
0; Mismatches 31; Indels
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Pred. No. 2.6e+02;
0; Mismatches 31; Indels
                        23; Indels
      Pred. No. 1.3e+02;
0; Mismatches 23
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US-09-270-767-20105/c
Sequence 20105, Application US/09270767
; Patent No. 6703491
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            ; TYPE: DNA
; ORGANISM: Drosophila melanogaster
US-09-270-767-20105
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1 Similarity 61.7%;
50; Conservative C
  66.78;
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Best Local Similarity 61.7%;
Matches 50; Conservative
Best Local Similarity 66.7
Matches 46; Conservative
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Best Local Similarity
Matches 50; Conserva
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LENGTH: 89
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1966 GCCTTGGAAGCAAAGGAGCTGGCCCGGCAGCAGCTCCGGGAGCAGCTGGACGAGGT 2021
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              Length 93;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         Indels
Sequence 24, Application US/08556978B
Fatent No. 6268169
GENERAL INFORMATION:
TITLE OF INVENTION:
NUMBER OF SEQUENCES:
NUMBER OF SEQUENCES:
ADDRESSEE: B. I DU PONT DE NEMOURS AND COMPANY
STREET: 1007 MARKET STREET
STREET: 1007 MARKET STREET
STATE: DELAMARE
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               ADDRESSEE: B. I. DU PONT DE NEMOURS AND COMPANY
STREET: 1007 MARKET STREET
CITY: ILMINITON
STATE: DELAWARE
COUNTRY: UNITED STATES OF AMERICA
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      GENERAL INFORMATION:
APPLICANT: PAHNESTOCK, STEPHEN F.
TITLE OF INVENTION: NOVEL RECOMBINANTLY PRODUCED
TITLE OF INVENTION: SPIDER SILK ANALOGS
NUMBER OF SEQUENCES: 107
CORRESPONDENCE ADDRESS:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            0.6%; Score 30.4; DB 3; 71.4%; Pred. No. 4.9e+02;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         0; Mismatches
                                                                                                                                                                                                                                                                                                                                       MEDIUM TYPE: DISKETTE, 3.50 INCH
COMPUTER: IBM PC COMPATIBLE
OPERATING SYSTEM: MICROSOFT WINDOWS 95
SOFTWARE: MICROSOFT WORD FOR WINDOWS 95
CURRENT APPLICATION DATA:
APPLICATION NUMBER: US/08/556,978B
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           CR-9389-A
                                                                                                                                                                                                                                                                            UNITED STATES OF AMERICA
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            CLASSIFICATION: 435
PRIOR APPLICATION DATA:
APPLICATION NUMBER: 08/077,600
FILING DATE: JUNE 15, 1993
ATTORNEY/AGENT INFORMATION:
NAME: FLOYD, LINDA AXAMETHY
REGISTRATION NUMBER: 33,692
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           MEDIUM TYPE: DISKETTE, 3.50 INCH COMPUTER: IBM PC COMPATIBLE
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   US-08-556-978B-25/c
; Sequence 25, Application US/08556978B
; Patent No. 6268169
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      REFERENCE/DOCKET NUMBER: CI
TELECOMMUNICATION INFORMATION:
TELEPHONE: 302-892-8112
TELEPAX: 302-773-0164
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              MOLECULE TYPE: DNA (genomic)
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           INFORMATION FOR SEQ ID NO: SEQUENCE CHARACTERISTICS:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         Matches 40; Conservative
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         LENGTH: 93 base pairs
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             nucleic acid
EDNESS: single
                                                                                                                                                                                                                                                                                                                       COMPUTER READABLE FORM:
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MEDIUM TYPE: DISKETT
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              Query Match
Best Local Similarity
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           linear
                                                                                                                                                                                                                                                                                            19898
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                            FILING DATE
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                                                                                                                                                                                                                                                                         COUNTRY:
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; Sequence 14585, Application US/09513999C; Patent No. 6783961
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                MOLECULE TYPE: other nucleic acid

DESCRIPTION: /desc = "synthetic"

US-08-068-747-1
                                                                                                                                                                                                                                                                                                                                                                                                       GENERAL INFORMATION:
APPLICANT: Dumas Milne Edwards, J.B.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           g, c or t
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Best Local Similarity 59.3%;
Matches 48; Conservative 1
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           ; OTHER INFORMATION: r=a or g
US-09-513-999C-14585
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           NAME/KEY: misc_feature
LOCATION: 40
OTHER INFORMATION: n=a, g
PEATURE:
NAME/KEY: misc_feature
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   ORGANISM: Homo sapiens
linear
                                                                                                                                                                                                                                                                                                               RESULT 12
US-09-513-999C-14585
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      US-07-814-220-26
TOPOLOGY:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             LOCATION:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 TYPE: DNA
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               APPLICANT: Schalling, Martin
APPLICANT: Hudson, Thomas J.
APPLICANT: Housman, David E.
TITLE OF INVENTION: Direct Determination of Expanded
TITLE OF INVENTION: Nucleotide Repeats in the Human Genome
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       Length 93;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               16; Indels
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 NUMBER OF SEQUENCES: 11
CORRESSONDENCE ADDRESS:
ADDRESSEE: Hamilton, Brook, Smith & Reynolds, P.C.
STREET: Two Militia Drive
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          COMPUTER READABLE FORM:
COMPUTER READABLE FORM:
MEDLUM TYPE: Floppy disk
COMPUTER: IBM PC Compatible
COMPUTER: IBM PC COMPATIBLE
COMPUTER: DEADER PC-DOS/MS-DOS
SOFTWARE: Patentin Release #1.0, Version #1.30
CURRENT APPLICATION DATA:
APPLICATION NUMBER: US/08/068,747
FILING DATE: 28-MAY.1993
CLASSIFICATION: 435
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  Query Match 0.6%; Score 30.4; DB 3; Best Local Similarity 71.4%; Pred. No. 4.9e+02; Matches 40; Conservative 0; Mismatches 16;
OPERATING SYSTEM: MICROSOFT WINDOWS 95
SOFTWARE: MICROSOFT WORD FOR WINDOWS 95
CURRENT APPLICATION DATA:
APPLICATION NUMBER: US/08/556,978B
                                                                                                                                                                                                                                                                          CR-9389-A
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   ATTORNEY AGENT INFORMATION:
NAME: Granahan, Patricia
REGISTRATION NUMBER: 32,227
REFERENCE/DOCKET NUMBER: MIT-6141
TELECOMMUNICATION INFORMATION:
TELEPHONE: 617-861-6240
                                                                                                            CLASSIFICATION: 435
PRIOR APPLICATION DATA:
APPLICATION NUMBER: 08/077,600
FILING DATE: JUNE 15, 1993
ATTORNEY/AGENT INFORMATION:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                US-08-068-747-1/c; Sequence 1, Application US/08068747; Patent No. 5695933; GENERAL INFORMATION:
                                                                                                                                                                                                                           NAME: FLOYD, LINDA AXAMETHY
REGISTRATION NUMBER: 33,692
REFERENCE/DOCKET NUMBER: CR
                                                                                                                                                                                                                                                                                          TELECOMMUNICATION INFORMATION: TELEPHONE: 302-892-8112
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   ; MOLECULE TYPE: DNA (genomic)
US-08-556-978B-25
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         TELEFAX: 617-861-9540
INFORMATION FOR SEQ ID NO: 1:
                                                                                                                                                                                                                                                                                                                                TELEFAX: 302-773-0164
INFORMATION FOR SEQ ID NO:
SEQUENCE CHARACTERISTICS:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    SEQUENCE CHARACTERISTICS:
LENGTH: 51 base pairs
                                                                                                                                                                                                                                                                                                                                                                                                                93 base pairs
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                TYPE: nucleic acid
STRANDEDNESS: single
                                                                                                                                                                                                                                                                                                                                                                                                                                 nucleic acid
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          CITY: Lexington
STATE: Massachusett
COUNTRY: USA
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                linear
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                                                                                              FILING DATE:
                                                                                                                                                                                                                                                                                                                                                                                                                LENGTH:
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1465 AAGCGGCAGCTGGAGCTGGAGAAGCAGCTGGAAGCAGCGGGAGCTGGAGCGGCGCAGCGA 1524
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                                                                                                                                                                                                                                                                                                                                                                                          APPLICANT: Duclert, A. APPLICANT: Duclert, A. APPLICANT: Giordano, J.Y.

APPLICANT: Giordano, J.Y.

TITLE OF INVENTION: Expressed Sequence Tags and Encoded Human Proteins. Patent No. 6783961

FILE REFERENCE: 59.US2.REG

CURRENT APPLICATION NUMBER: US 60/122,487

PRIOR FILING DATE: 1999-02-26

NUMBER OF SEQ ID NOS: 36681

SEQ ID NO 14885

LENGTH: 86
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                                                      0; Gaps
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GENERAL INFORMATION:

GENERAL INFORMATION:

APPLICANT: Cacci, Thomas E.

APPLICANT: Szumanski, Maria B.W.

TITLE OF INVENTION: SYNTHETIC GENE CODING FOR ITS PRODUCTION

TITLE OF INVENTION: SYNTHETIC GENE CODING FOR ITS PRODUCTION

NUMBER OF SEQUENCES: 43

CORRESPONDENCE ADDRESS:

ADDRESSEE: WHITHAM, CURTIS & WHITHAM

STREET: Suite 900

STREET: Suite 900
                                                                                                       1471 CAGCTGGAGCTGGAGAAGCAGCTGGAGAAGCAGCGGGAGCTGGAGCGGCAG 1521
                                                                                                                                                        Query Match 0.6%; Score 30.2; DB 1; Length 51; Best Local Similarity 74.5%; Pred. No. 3.7e+02; Matches 38; Conservative 0; Mismatches 13; Indels
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          Score 30; DB 4; Length 86;
Pred. No. 6e+02;
1; Mismatches 32; Indels
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-hes 32; Indels
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NAME: Whitham, Michael E.
REGISTRATION NUMBER: 32,635
REFERCNEW/DOCKET NUMBER: CIT.
TELECOMMUNICATION INFORMATION:
TELEPHONE: 703-391-2510
TELEFAX: 703-391-9035
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                INFORMATION FOR SEQ ID NO: 2
SEQUENCE CHARACTERISTICS:
LENGTH: 6.2 base pairs
TYPE: nucleic acid
STRANDEDNESS: double
ATTORNEY/AGENT INFORMATION
                                                                                                                                                        INFORMATION FOR SEQ ID NO:
SEQUENCE CHARACTERISTICS:
LENGTH: 57 base pairs
TYPE: nucleic acid
STRANDEDNESS: double
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 703-391-9035
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              STREET: Suite
CITY: Reston
STATE: VA
COUNTRY: USA
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   MOLECULE TYPE:
DESCRIPTION:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              RESULT 15
US-07-814-220-25/c
                                                                                                                                                                                                                                                                                                                                                     US-07-812-421-26
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APPLICANT: Caceci, Thomas
APPLICANT: Toth, Thomas
APPLICANT: Stumminski, Maria B.W.
TITLE OF INVENTION: SYNTHETIC GENE CODING FOR ITS PRODUCTION
NUMBER OF SEQUENCES: 43
CORRESPONDENCE ADDRESS:
ADDRESSEE MILTHAM, CURTIS & WHITHAM
STREET: Rescon Intl. Center, 11800 Sunrise Valley Dr.,
STREET: Suite 900
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         Query Match
0.6%; Score 29.4; DB 2; Length 57;
Best Local Similarity 70.9%; Pred. No. 6.6e+02;
Matches 39; Conservative 0; Mismatches 16; Indels
                                                                            COMPUTER READABLE FORM:
MEDIUM TYPE: Floppy disk
COMPUTER: IBM PC compatible
COMPUTER: TEM PC compatible
OPERATING SYSTEM: PC-DOS/MS-DOS
SOFTWARE: PatentIn Release #1.0, Version #1.30
CURRENT APPLICATION DATA:
APPLICATION NUMBER: US/07/814,220
FILING DATE: 23-DEC-1991
CLASSIFICATION 1435
PRIOR APPLICATION NUMBER: US 07/588,437
FILING DATE: 25-SEP-1990
ATTONENTATION NUMBER: US 07/588,437
FILING DATE: 25-SEP-1990
ATTONENTATION NUMBER: US 07/588,437
FILING DATE: 25-SEP-1990
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    COMPUTER READABLE FORM:
MEDIUM TYPE: Floppy disk
COMPUTER: IBM PC compatible
OPERATING SYSTEM: PC-DOS/MS-DOS
SOFTWARE: Patentin Release #1.0, Version #1.30
CURRENT APPLICATION DATA:
APPLICATION NUMBER: US/07/812,421
FILING DATE: 23-DEC-1991
CLASSIFICATION 1435
PRIOR APPLICATION DATA:
APPLICATION NUMBER: US 07/588,437
FILING DATE: 25-SEP-1990
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                other nucleic acid
/desc = "synthetic DNA"
                                                                                                                                                                                                                                                                                                                                                                                     NAME: Whitham, Michael B.
REGISTRATION NUMBER: 32,635
REFRENCE/POCKET NUMBER: CIT.016
TELECOMMUNICATION INFORMATION:
TELECHONE: 703-391-210
TELEFAX: 703-391-9035
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      Sequence 26, Application US/07812421 Patent No. 5932697
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            TELEFAX: 703-391-9035
INFORMATION FOR SEQ ID NO: 2.
SEQUENCE CHARACTERISTICS:
LENGTH: 57 base pairs
TYPE: nucleic acid
STRANDEDNESS: double
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               linear
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  CITY: Reston
STATE: VA
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              MOLECULE TYPE:

DESCRIPTION:

US-07-814-220-26
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                                                           20191
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US-07-812-421-26
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1468 CGGCAGCTGGAGCTGGAGAAGCAGCTGGAGAAGCAGCGGGAGCTGGAGCGGCAGC 1522
                                                                                                                                                                                                                     0; Gaps
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GENERAL INFORMATION:

APPLICANT: Cacei, Thomas

APPLICANT: Toth, Thomas

APPLICANT: Szumanski, Maria B.W.

APPLICANT: Syntheric Gene Coding for ITS PRODUCTION

NUMBER OF INVENTION: SYNTHETIC GENE CODING FOR ITS PRODUCTION

NUMBER OF SEQUENCES: 43

CORREGEOUBRICES: 43

STREET: Reston Intl. Center, 11800 Sunrise Valley Dr.,

STREET: Suite 900
                                                                                                                                                          Length 57;
                                                                                                                                                                                                                  Indels
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     CURRENT APPLICATION DATA:
CURRENT APPLICATION DATA:
APPLICATION NUMBER: US/07/814,220
FILING DATE: 23-DEC-1991
FILING DATE: 23-DEC-1991
FILING DATE: 25-DEC-1991
FILING DATE: 25-DE-1990
ATTORNEY/AGENT INFORMATION:
NAME: Whitham, Michael E.
REGISTRATION NUMBER: 32,635
REFERENCE/DOCKET NUMBER: GIT.016
TELECOMMUNICATION INFORMATION:
TELECOMMUNICATION INFORMATION:
TELECOMMUNICATION INFORMATION:
TELECOMMUNICATION INFORMATION:
                                                                                                                                                                                                                        16;
                                                                                                                                                    Query Match
0.6%; Score 29.4; DB 2;
Best Local Similarity 70.9%; Pred. No. 6.6e+02;
Matches 39; Conservative 0; Mismatches 16;
TOPOLOGY: linear
MOLECULE TYPE: other nucleic acid
DESCRIPTION: /desc = "synthetic DNA"
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  /desc = "synthetic DNA"
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COMPUTER READABLE FORM:
MEDIUM TYPE: Floppy disk
COMPUTER: ISM PC compatible
OPERATING SYSTEM: PC-DOS/MS-DOS
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Ouery Match 0.6%; Score 29.4; DB 2; Length 62;
Best Local Similarity 70.9%; Pred. No. 6.9e+02;
Matches 39; Conservative 0; Mismatches 16; Indels 0; Gaps
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ò qq Search completed: April 29, 2005, 02:23:45 Job time: 762.328 secs

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April 28, 2005, 07:33:31; Search time 2706.88 Seconds (without alignments) 11433.739 Million cell updates/sec
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             Published Applications NA:*

1: /cgn2_6/ptodata/1/pubpna/USO7_PUBCOMB.seq:*
2: /cgn2_6/ptodata/1/pubpna/PCT_NWW_PUBLs.seq:*
3: /cgn2_6/ptodata/1/pubpna/USO6_NWW_PUBLs.seq:*
4: /cgn2_6/ptodata/1/pubpna/USO6_PUBCOMB.seq:*
5: /cgn2_6/ptodata/1/pubpna/USO7_NWW_PUB.seq:*
6: /cgn2_6/ptodata/1/pubpna/PCTUS_PUBCOMB.seq:*
7: /cgn2_6/ptodata/1/pubpna/PCTUS_PUBCOMB.seq:*
8: /cgn2_6/ptodata/1/pubpna/USO9_PUBCOMB.seq:*
9: /cgn2_6/ptodata/1/pubpna/USO9_PUBCOMB.seq:*
10: /cgn2_6/ptodata/1/pubpna/USO9_PUBCOMB.seq:*
11: /cgn2_6/ptodata/1/pubpna/USO9_PUBCOMB.seq:*
12: /cgn2_6/ptodata/1/pubpna/USO9_NWW_PUB.seq:*
13: /cgn2_6/ptodata/1/pubpna/USO9_NWW_PUB.seq:*
14: /cgn2_6/ptodata/1/pubpna/USO9_NWW_PUB.seq:*
15: /cgn2_6/ptodata/1/pubpna/USIOR_PUBCOMB.seq:*
16: /cgn2_6/ptodata/1/pubpna/USIOR_PUBCOMB.seq:*
16: /cgn2_6/ptodata/1/pubpna/USIOR_PUBCOMB.seq:*
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/cgn2_6/ptodata/1/pubpna/US10E_PUBCOMB.seq
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GenCore version 5.1.6
Copyright (c) 1993 - 2005 Compugen Ltd.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        Total number of hits satisfying chosen parameters:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      5642217 segs, 3043843248 residues
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                Post-processing: Minimum Match 0%
Maximum Match 100%
Listing first 45 summaries
                                                                                                               OM nucleic - nucleic search, using sw model
                                                                                                                                                                                                                                                                                                                                                                                                             IDENTITY NUC
Gapop 10.0 , Gapext 1.0
                                                                                                                                                                                                                                                                                          US-09-674-237B-1
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         Minimum DB seq length: 0
Maximum DB seq length: 100
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                                                                                                                                                                                                                                                                                                                      Perfect score:
                                                                                                                                                                                                                                                                                                                                                        Sequence:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      Searched:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         Database
                                                                                                                                                                          Run on:
                                                                                                                                                                                                                                                                                          Title:
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Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

. Description	Sequence 27224, A	Sequence 1543, Ap	Sequence 10766, A	Sequence 463, App	Sequence 463, App	Sequence 6, Appli	Sequence 8, Appli	Sequence 24680, A	Sequence 156, App	Sequence 462, App	Sequence 462, App
SUMMARIES ID	US-09-908-975-27224	US-09-908-975-1543	US-09-908-975-10766	US-09-854-867-463	US-10-786-970A-463	US-10-333-894A-6	US-10-407-818-8	US-09-864-761-24680	US-10-759-731A-156	US-09-854-867-462	US-10-786-970A-462
DB	10	10	10	10	19		18	6	19	10	19
* Query = Match Length DB	65	65	9	69	69	87	63	93	87	69	69
* Query Match	1.3	1.1	1.0	0.7	0.7	0.7	0.7	0.7	9.0	9.0	9.0
Score	65	54	48.8	37.6	37.6	36.6	34.6	33.4	32.4	32.2	32.2
Result No.	-	8	m	4	5	9	7	დ ს	ο Ο	10	11

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0-758-307-66 0-852-797-339 0-055-96-174 0-029-386-17340 0-759-731A-155 0-061-201-11	2 2 2 2 2 2 2 4 3 2 5 4 5 4 3 4 3 4 3 4 3 4 3 4 3 4 3 4 3 4	10-323-051-21 10-088-36-3 10-021-323-14266 10-021-323-15706 10-021-323-15706 10-865-478-506 10-275-071-15	0.094-578-65 0.096-986-58 9.854-867-468 0.786-970A,468 0.645-471A-31 0.260-238-2343 0.260-238-2343 0.023-066A-66 0.021-323-808 9-738-937-14
0-758-307-6 0-852-797-3 0-085-906-1 0-029-386-1 0-759-731A-1 0-061-201-1	0-023-500-10 9-373-658-5 9-373-658-5 0-759-731A-5 0-023-066A- 0-804-678-5 0-021-323-1	0-323-051-2 0-488-936-2 0-021-323-1 0-021-323-1 0-021-323-1 0-865-478-5 0-275-071-1	-804-67 -996-996-996-996-996-996-996-996-996-99
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## ALIGNMENTS

Sequence 27224, Application US/09908975
; Sequence 27224, Application US/09908975
; Publication No. US20030165843A1
; GENERAL INPORMATION:
 APPLICANT: WASSERMAN, Alon
; APPLICANT: WASSERMAN, Alon
; APPLICANT: MINTZ, Eliat
; APPLICANT: FAIGLER, Simchon
; TITLE OF INVENTION: OLIGONUCLEOTIDE LIBRARY FOR DETECTING RNA TRANSCRIPTS AND SPLICE N
; TITLE OF INVENTION: OLIGONUCLEOTIDE LIBRARY FOR DETECTING RNA TRANSCRIPTS AND SPLICE N
; TITLE OF INVENTION: THAT POPULATE A TRANSCRIPTOME
; TITLE OF INVENTION: THAT POPULATE A TRANSCRIPTOME
; FILE REFERENCE: 36688-005
; CURRENT FILING DATE: 2001-07-20
; PRIOR APPLICATION NUMBER: US 60/221,607
; PRIOR PLING DATE: 2000-07-28
; NUMBER OF SEQ ID NOS: 32337
; SGOTWARE: PARCHIN VERSION 3.0
; SEQ ID NO 27224
LENGTH: 65 Length 65; ; ORGANISM: Mus musculus US-09-908-975-27224

4058 GCAGTTTACCTCATTTGACCTTAGTTGCATGTGATGACAATGTCTGAGTCACTGCGTGCA 4117 Gaps ö 1.3%; Score 65; DB 10; Length 65 100.0%; Pred. No. 1e-07; tive 0; Mismatches 0; Indels Query Match 1.3 Best Local Similarity 100. Matches 65; Conservative

1 GCAGTTTACCTCATTTGACCTTAGTTGCATGTCGAAATGTCTGAGTCACTGCGTGCA

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GENERAL INFORMATION:
GENERAL INFORMATION:
APPLICANT: GOAN, KNOLL
APPLICANT: ROGAN, PETER K
TITLE OF INVENTION: SINGLE COPY GENOMIC HYBRIDIZATION PROBES AND METHOD OF GENERATING
FILE REFERENCE: 30307
CURRENT APPLICATION
CURRENT PILING DATE: 2003-05-08
NUMBER OF SEQ ID NOS: 613
SOFTWARE: PATENTIN Version 3.1
SEQ ID NO 463
LENGTH: 69
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     Sequence 463, Application US/10786970A

Publication No. US2005064449A1

Publication No. US20050064449A1

APPLICANT: ADAN, KNOLL

APPLICANT: ROGAN, PETER

TITLE OF INVENTION: SINGLE COPY GENOMIC HYBRIDIZATION PROBES AND METHOD OF GENERATING

FILE REFERENCE: 30307

CURRENT PILING DATE: 2004-02-24

PRIOR FILING DATE: 2004-05-16

NUMBER OF SEQ ID NOS: 479

SOFTWARE: Patentin version 3.0

SEQ ID NO 463
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            CTHER INFORMATION: Description of Artificial Sequence: repetitive sequence found in CTHER INFORMATION: many eutherial genomes. Length of core repeating element is vari; CTHER INFORMATION: able and is often polymorphi US-10-786-970A-463
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           OTHER INFORMATION: Description of Artificial Sequence: repetitive sequence found in OTHER INFORMATION: many entherial genomes. Length of core repeating element is varioTHER INFORMATION: able and is often polymorphic
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Length 60;
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            Query Match 0.7%; Score 37.6; DB 10; Length Best Local Similarity 72.1%; Pred. No. 6.6; Matches 49; Conservative 0; Mismatches 19; Indels
                                           Indels
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               Query Match 0.7%; Score 37.6; DB 19;
Best Local Similarity 72.1%; Pred. No. 6.6;
Matches 49; Conservative 0; Mismatches 19;
  Score 48.8; DB 10;
Pred. No. 0.0039;
0; Mismatches 7;
                                                                                                                                                                                                                   Sequence 463, Application US/09854867
Publication No. US20030224356A1
                                                                                                                                                                                                                                                                                                                                                                                                                                                                              TYPE: DNA ORGANISM: Artificial Sequence
      1.0%;
        Query Match
Best Local Similarity 88.3
Matches 53; Conservative
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             US-10-786-970A-463
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                                                                                                                                                          APPLICANT: SHORHAN, Avi
APPLICANT: WASSERMAN, Alon
APPLICANT: MINIZ, Eli
APPLICANT: MINIZ, Eli
APPLICANT: MINIZ, Eli
APPLICANT: MINIZ, Liat
APPLICANT: NUMBER: US 6099,975
CURRENT APPLICATION NUMBER: US 60/287,724
PRIOR FILING DATE: 2001-07-20
PRIOR FILING DATE: 2000-07-28
PRIOR FILING DATE: 2000-07-28
NUMBER OF SEQ ID NOS: 32337
SOFUTANE: Patentin version 3.0
LENGTH: 60
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        ; Sequence 10766, Application US/09908975
; Publication No. US20030165843A1
; GENERAL INFORMATION:
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         TYPE: DNA
ORGANISM: Rattus norvegicus
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Best Local Similarity 98.5
Matches 65; Conservative
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US-09-908-975-10766
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                                  4118 GAGGC 4122
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US-09-908-975-10766
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US-10-407-818-8
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                  1455 GCAGGAGGCCCAAGCGCCAGCTGGAGCTGGAGCAGCTGGAGAAGCAGCGGGAGCTGGA 1514
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                                                         Sequence 8, Application US/10407818;
Publication No. US20040198971A1
GENERAL INFORMATION:
APPLICANT: STAVELANOPOULOS, JANNIS G.
APPLICANT: DONGGAN, JAMES J.
TITLE OF INVENTION: MULTISIGNAL LABELING REAGENTS, AND PROCESSES AND USES;
TITLE OF INVENTION: THEREFOR
FILE REPRERENCE: ENZ-65
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                Gaps
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           ; OTHER INFORMATION: Description of Artificial Sequence:/note = ; OTHER INFORMATION: synthetic construct
US-10-333-894A-6
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       DB 18; Length 87;
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                                                                                                                                                                                                                                                                                                                         APPLICANT: Chang, Chawnahang
APPLICANT: Chang, Chawnahang
APPLICANT: Haing, Ann
TITLE OF INVENTION: PROSTATE CANCER
FILE REFERENCE: 21108.0001U1
CURRENT APPLICATION NUMBER: US/10/333,894A
CURRENT FILING DATE: 2003-01-24
SOFTWARE: FASTSEQ for Windows Version 4.0
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     Query Match 0.7%; Score 36.6; DB 18; Length E
Best Local Similarity 65.1%; Pred. No. 15;
Matches 54; Conservative 0; Mismatches 29; Indels
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 CURRENT APPLICATION UNBER: US/10/407,818
CURRENT FILING DATE: 2003-04-03
NUMBER OF SEQ ID NOS: 16
SEQ ID NO 8
LENGTH: 63
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                                                                                                                                                                                                                                                        Sequence 6, Application US/10333894A, Publication No. US20040259085A1, GENERAL INFORMATION:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          FEATURE:
OTHER INFORMATION: 3'-amidated
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             TYPE: DNA
ORGANISM: Artificial Sequence
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ORGANISM: Artificial Sequence
                                                                                                       1515 GCGGCAGC 1522
                                                                                                                                                 GCAGCAGC 68
                                                                                                                                                                                                                                      US-10-333-894A-6
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    US-10-407-818-8
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 SEQ ID NO 6
LENGTH: 87
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RESULT 8
US-09-864-761-24680/c
US-09-864-761-24680, Application US/09864761
; Sequence 20020048763A1
; Fatent No. US2002048763A1
; GENERAL INFORMATION:
; APPLICANT: Rank, David R.
; APPLICANT: Rank, David K.
; APPLICANT: Chen, Wensheng
; TITLE OF INVENTION: HUMAN GENOME-DERIVED SINGLE EXON NUCLEIC ACID PROBES USEFUL FOR TITLE OF INVENTION: GENE EXPRESSION ANALYSIS BY MICROARRAY
                                                                                ö
                                                                                                                                                        1466 AGCGGCAGCTGGAGCTGGAGCAGCTGGAGAAGCAGCGGGAGCTGGAGCGGCAGC 1522
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        63;
        Length
                                                                                Indels
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PRIOR APPLICATION UNMER: US 60/180,312
PRIOR PILING DATE: 2000-02-04

PRIOR FILING DATE: 2000-02-04

PRIOR PILING DATE: 2000-02-26

PRIOR PILING DATE: 2000-08-03

PRIOR PILING DATE: 2000-10-04

PRIOR PILING DATE: 2000-10-04

PRIOR PILING DATE: 2001-10-04

PRIOR PILING DATE: 2001-01-30

PRIOR PILING DATE: 2001-03-30

PRIOR APPLICATION NUMBER: US 09/704, 203

PRIOR PILING DATE: 2001-03-30

PRIOR PILI
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OTHER INFORMATION: EXPRESSED IN LUNG, SIGNAL = 2.8

OTHER INFORMATION: EXPRESSED IN PLACENTA, SIGNAL = 2.4

OTHER INFORMATION: EXPRESSED IN ADULT LIVER, SIGNAL = OTHER INFORMATION: EXPRESSED IN HELA, SIGNAL = 3.5
Score 34.6; DB 18;
Pred. No. 45;
0; Mismatches 14;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          FILE REFERENCE: Aeomica-X-1
CURRENT APPLICATION NUMBER: US/09/864,761
CURRENT FILING DATE: 2001-05-23
Query Match 0.7%;
Best Local Similarity 75.4%;
Matches 43; Conservative
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RESULT 10
US-09-854-867-462
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                                                                                                                                                                                                                                                                                                                                       Query Match 0.7%; Score 33.4; DB 9; Length 93; Best Local Similarity 72.9%; Pred. No. 1.3e+02; Matches 43; Conservative 0; Mismatches 16; Indels
CTHER INFORMATION: EXPRESSED IN BRAIN, SIGNAL = 3.9

CTHER INFORMATION: EXPRESSED IN BONE MARROW, SIGNAL = 4.5

OTHER INFORMATION: EXPRESSED IN HEART, SIGNAL = 4.6

CTHER INFORMATION: EXPRESSED IN FEARL LUVER, SIGNAL = 4.6

OTHER INFORMATION: NT HIT: g15031896, EVALUE 2.00e-13

OTHER INFORMATION: BST_HUMAN HIT: R18580.1, EVALUE 3.00e-13

US-09-864-761-24680
                                                                                                                                                                                                                                                                                                                                                                                                                                                                US-10-759-731A-156/c
| Sequence 156, Application US/10759731A|
| Sequence 156, Application US/10759731A|
| Publication No. US20050079574A1|
| GENERAL INFORMATION:
| APPLICANT: Bond, Christoper J. TITLE OF INVENTION: SYMTHETIC ANTIBODY PHAGE LIBRARIES FILE REFERENCE: 11669.136USU1 |
| CURRENT APPLICATION: SYMTHETIC ANTIBODY PHAGE LIBRARIES |
| FURRENT FILING DATE: 2004-01-16 |
| PRIOR APPLICATION NUMBER: US 60/441,059 |
| PRIOR PILING DATE: 2003-01-16 |
| PRIOR PILING DATE: 2003-10-16 |
| PRIOR FILING DATE: 2003-10-08 |
| PRIOR FILING DATE: 2003-10-08 |
| SOFTWARE: PATENT: 2003-10-08 |
| SOFTWARE: PATENT: VERSION 3.3 |
| SEQ ID NO.156 |
| LENGTH: 87
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         OTHER INFORMATION: VLK ala scan
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      LOCATION: (41)...(41)
OTHER INFORMATION: 8 is g or c
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             TYPE: DNA
ORGANISM: Artificial Sequence
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OTHER INFORMATION: y is c or
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OTHER INFORMATION: s is g or
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NAME/KEY: misc_feature
LOCATION: (37)..(38)
OTHER INFORMATION: 8 is g
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OTHER INFORMATION: y is c
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LOCATION: (28)..(28)
OTHER INFORMATION: s is g
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OTHER INFORMATION: r is FEATURE:
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LOCATION: (34)..(35)
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1454 AGCAGGAGGCCAAGCGGCAGCTGGAGCTGGAAGCAGCTGGAGAAGCAGCGGGAGCTGG 1513
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Best Local Similarity 41.9%; Pred. No. 2.3e+02;
Matches 36; Conservative 22; Mismatches 28;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                1514 AGCGCCAGCGAGAGGAGGAGGAGG 1539
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LOCATION: (59)..(59)
OTHER INFORMATION: y is c or t
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OTHER INFORMATION: s is g or c
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NAME/KEY: misc feature
LOCATION: (43)...(43)
OTHER INFORMATION: k is g or t
                                                                                                                                                                                 NAME/KEY: misc feature
LOCATION: (50)...(50)
OTHER INFORMATION: y is c or t
                                                                                                                                                                                                                                                                                                   LOCATION: (53)...(53)
OTHER INFORMATION: s is g or c
                                                                                                                                                                                                                                                                                                                                                                                           LOCATION: (55)...(55)
OTHER INFORMATION: r is a or g
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THER INFORMATION: 8 is g or c
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OTHER INFORMATION: y is c or t
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OTHER INFORMATION: m is a or c
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OTHER INFORMATION: y is c or t
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OTHER INFORMATION: r is a or g
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LOCATION: (58)..(58)
OTHER INFORMATION: k is g
                                                                                                                    LOCATION: (46)...(46)
OTHER INFORMATION: k is g
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                                                                                          NAME/KEY: misc_feature
LOCATION: (46)..(46)
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1444 GAGCGCCAGGAGCAGGAGGCCAACCGGCAGCTGGAGCTGGAGAAGCAGCTGGAGAAGCAG 1503
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       Sequence 339, Application US/10852797
Publication No. US20050064455A1
GENERAL INFORMATION:
APPLICANT: Genomic Health, Inc.
APPLICANT: Miler, Kathy D.
APPLICANT: Miler, Kathy D.
APPLICANT: Sledge, George
APPLICANT: Sledge, George
APPLICANT: Soule, Sharon
TITLE OF INVENTION: Gene Expression Markers for Predicting
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             IndelB
                                                                                                     APPLICANT: GENOMIC HEALTH, INC.
APPLICANT: GENOMIC HEALTH, INC.
APPLICANT: Coblegh, Melody
APPLICANT: Coblegh, Melody
APPLICANT: Coblegh, Melody
APPLICANT: Baker, Joffree
APPLICANT: Cronin, Maureen
TITLE OF INVENTION: GENE EXPRESSION MARKERS FOR BREAST
TITLE OF INVENTION: CANCER PROGNOSIS
FILE REFERENCE: 39740/0008 US
CURRENT APPLICATION NUMBER: US 60/440,861
PRIOR PILING DATE: 2004-01-15
NUMBER OF SEQ ID NOS: 440
SEQ ID NOS: 440
SEQ ID NOS: False SEQ for Windows Version 4.0
SEQ ID NO 66
LENGTH: 77
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   Query Match 0.6%; Score 31.2; DB 18; Best Local Similarity 70.0%; Pred. No. 4.7e+02; Matches 42; Conservative 0; Mismatches 18;
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70.0%; Pred. No. 4.7e+02;
iive 0; Mismatches 18;
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CURRENT APPLICATION NUMBER: US/10/852,797
CURRENT FILING DATE: 2004-05-24
FRIOR APPLICATION NUMBER: 60/473,970
PRIOR FILING DATE: 2003-05-28
NUMBER OF SEQ ID NOS: 372
SOFTWARE: FastSEQ for Windows Version 4.0
; SEQ ID NO 339
                                Sequence 66, Application US/10758307
Publication No. US20040209290A1
GENERAL INFORMATION:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     ORGANISM: Artificial Sequence
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               TYPE: DNA ORGANISM: Artificial Sequence
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         ; OTHER INFORMATION: Amplicon US-10-758-307-66
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US-10-852-797-339
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Matches '42; Conservative
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        US-10-758-307-66
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                                                                         APPLICANT: JOAN, KNOLL H
APPLICANT: JOAN, KNOLL H
APPLICANT: GOGAN, PETER K
TITLE OF INVENTION: SINGLE COPY GENOMIC HYBRIDIZATION PROBES AND METHOD OF GENERATING
FILE REFERENCE: 30307
CURRENT APPLICATION WUMBER: US/09/854,867
CURRENT FILING DATE: 2003-05-08
NUMBER OF SEQ ID NOS: 613
SOFTWARE: Patentin version 3.1
SEQ ID NO 462
LENGTH: 69
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         Segrible Application US/10786970A

Series Application US/10786970A

Publication No. US20050064449A1

GENERAL INFORMATION:
GENERAL INFORMATION:
APPLICANT: JOAN, KNOLL
APPLICANT: GOGAN, PETER
TITLE OF INVENTION: SINGLE COPY GENOMIC HYBRIDIZATION PROBES AND METHOD OF GENERATING CURRENT FILING DATE: 2004-02-24

PRIOR APPLICATION NUMBER: US/10/786, 970A
CURRENT FILING DATE: 2000-05-16

NUMBER OF SEQ ID NOS: 479

SOFTWARE: Patentin version 3.0

SEQ ID NO 462
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            FEATURE:
CTHER INFORMATION: Description of Artificial Sequence: repetitive sequence found in OTHER INFORMATION: many eutherial genomes. Length of core repeating element is variated US-10-786-970A-462
                                                                                                                                                                                                                                                                                                                                                                                                                       OTHER INFORMATION: Description of Artificial Sequence: repetitive sequence found in CHER INFORMATION: many eutherial genomes. Length of core repeating element is varia; OTHER INFORMATION: ble and is often polymorphic US-09-854-867-462
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Pred. No. 2.3e+02;
0; Mismatches 23; IndelB
Sequence 462, Application US/09854867
Publication No. US20030224356A1
GENERAL INFORMATION:
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Best Local Similarity 66.7*
....hes 46; Conservative
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US-10-786-970A-462
                                                                                                                                                                                                                                                                                                                                                TYPE: DNA
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Search completed: April 29, 2005, 03:41:18 Job time: 2708.88 secs
                                                                          1487 AGCAGCTGGAGAAG 1500
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APPLICANT: Penn, Sharron G.
APPLICANT: Rank, David R.
APPLICANT: Rank, David R.
APPLICANT: Rank, David R.
APPLICANT: HARZEL, David R.
TITLE OF INVENTION: HUMAN GENOME-DERIVED SINGLE EXON NUCLEIC ACID PROBES USEFUL FOR TITLE OF INVENTION: EXPRESSION ANALYSIS TWO
FILE REFERENCE: AEOMICA-X-2
CURRENT APPLICATION NUMBER: US/10/029,386
NUMBER OF SEQ ID NOS: 34288
SOFTWARE: Annomax Sequence Listing Engine vers. 1.1
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              Gaps
                                                                                                                                                                              APPLICANT: Gray, Gary S.

TITLE OF INVENTION: POLYMORPHIC ELEMENTS IN THE
TITLE OF INVENTION: POLYMORPHIC ELEMENTS IN THE
TITLE OF INVENTION: COSTIMULATORY RECEPTOR LOCUS AND USES THEREOF
CURRENT APPLICATION NUMBER: US/10/085,906
CURRENT APPLICATION NUMBER: US 60/126,215
PRIOR PELLOR DATE: 1999-03-25
PRIOR APPLICATION NUMBER: US 99/534,061
PRIOR PILING DATE: 2000-03-24
PRIOR APPLICATION NUMBER: PCT/US00/07938
PRIOR PILING DATE: 2000-03-24
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        Query Match 0.6%; Score 31.2; DB 14; Length 86; Best Local Similarity 60.7%; Pred. No. 5e+02; Matches 51; Conservative 0; Mismatches 33; Indels
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    NUMBER OF SEQ ID NOS: 545
SOFTWARE: FastSEQ for Windows Version 4.0
SEQ ID NO 174
LENGTH: 86
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 1537 AGGAAGGAGATCGAGAGGCGCGAG 1560
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                ; Sequence 17340, Application US/10029386
; Publication No. US20030194704A1
; GENERAL INFORMATION:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               FEATURE:
OTHER INFORMATION: MAP TO AL135920.4
OTHER INFORMATION: EXPRESSED IN BONE
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     25 AAGGGAGAGAGGAGAGGAGAG 2
                                             Sequence 174, Application US/10085906; Publication No. US20030054371A1
GENERAL INFORMATION:
APPLICANT: Ying, Vincent
APPLICANT: Wu, Paul
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 TYPE: DNA
ORGANISM: Homo sapiens
US-10-085-906-174
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ORGANISM: Homo sapiens
RESULT 14
US-10-085-906-174/c
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LENGTH: 99
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1427 AGGAGAGGAAAAGAGCGCGGGGGCGAGGAGCAGGCCAAGCGGCAGCTGGAGCTGGAGA 1486

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AX384806 Sequence
AX159551 Sequence
AX039312 Sequence
AX039312 Sequence
AX039521 Sequence
AX039521 Sequence
CQ185550 Sequence
CQ153723 Sequence
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CQ153723 Sequence
CQ25698 Sequence
CQ274588 Sequence
CQ274588 Sequence
CQ311642 Sequence
CQ37458 Sequence
CQ37458 Sequence
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CQ37630 Sequence
CQ37630 Sequence
AX25367 Sequence
AX25367 Sequence
AX039523 Sequence
AX039523 Sequence
AX039523 Sequence
AX039524 Sequence
AX039524 Sequence
AX039524 Sequence

Run

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Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Buteleostomi;
Mammalia; Eutheria; Primates; Catarrhini; Hominidae; Homo.
                                                                                                                                                                                                                                                                                                                                                                          Shoshan, A., Wasserman, A., Mintz, E., Mintz, L. and Faigler, S. Oligonucleotide library for detecting rna transcripts and splice variants that populate a transcriptome Patent: WO 0210449-A 10766 07-FEB-2002;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   CQ541131 60 bp DNA Sequence 10766 from Patent WO0210449.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          Synthetic transmembrane components.
1 B270475
1 B270475.1 G1:33080243
JP 2002541845-A/9.
8ynthetic construct
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88.3%; Pred. No. 5.1;
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0; Mismatches
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/organism="Homo sapiens"
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                                                         AR159550
CQ080578
CQ114850
CQ186430
CQ236983
CQ274588
CQ274588
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                                 AX039521
AY225366
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CQ877372
BD270481
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AX039523
BD270482
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Location/Qualifiers
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                                                                                                                                                                                                                                                                                                                                 Homo sapiens (human)
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                                                                                                                                                                                                                                                                                                                                          Homo sapiens
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Best Local Similarity
Matches 53; Conserv
DEFINITION
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                                                       April 28, 2005, 06:15:47; Search time 15157.7 Seconds (without alignments) 11642.487 Million cell updates/sec
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BD270475 Synthetic
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AJ388053 Hyla chry
AF143273 Vitis vin
BD270480 Synthetic
AX039313 Sequence
AX039522 Sequence
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BD270477
AX039310
AX039519
BD270478
AX039311
AX039520
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AX039517
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       GenCore version 5.1.6
(c) 1993 - 2005 Compugen Ltd.
                                                                                                                                                     4708233 segs, 24227607955 residues
                                                                                                                                                                       Total number of hits satisfying chosen parameters:
                                                                                                                                                                                                                                                                                                                                                                                                                              SUMMARIES
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Maximum Match 100%
Listing first 45 summaries
                                         nucleic search, using sw model
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AX039520
AR159552
HCH388053
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AX039309
AX039518
BD270477
AX039310
AX039519
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                                                                                                                             IDENTITY NUC Gapop 10.0 , Gapext 1.0
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Maximum DB seq length: 100
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Length 60 Indels 60

PAT 17-JUL-2003

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PAT 18-NOV-2000

AUTHORS TITLE JOURNAL

COMMENT

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1186 GAGCGCCAGGAGCAGGAGGCCAAGCGGCAGCTGGAGCAGGAAGCAGCTGGAGAAGCAG
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AG1P37/06,AG1P37/08,C07K14/705,C12N1/15,C12N1/19,C12N1/21, PC
88 GAGCAGCAGGAGCAGCAGCAGTAGCAGTAGCAGCAGCAGCAGCAGGAGCAGCAGGAGCAGGAG
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PF 17-APR-2000 JP 2000612453
PF 16-APR-1999 GB 9908816.3,16-APR-1999 GB 9908816
PALASTAIR DAVID GRIFFITHS LARWSON, HELENE MARGARET FINNEX PC
C12N15/09,A61K38/00,A61K48/00,A61P1/00,A61P3/10,A61P7/06,
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               Length 98;
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2e+02;
27;
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1 (bases 1 to 100)

Lawson, A.D.G. and Finney, H.M.
Synthetic transmembrane components
Patent: JP 2002541845-A 10 10-DEC-2002;
CELLTECH THERAPEUTICS LTD
OS Artificial Sequence
PN JP 2002541845-A/10
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           Score 41.8; DB 6;
Pred. No. 2e+02;
0; Mismatches 27;
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/organism="synthetic construct"
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                                                                                                                                                                                                                                                                                                          other sequences; artificial sequences
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                                                                                                                                                                                                                                                                                                                                                                  Synthetic transmembrane components Patent: WO 0063374-A 9 26-OCT-2000; CELLTECH THERAPEUTICS LIMITED (GB) Location/Qualifiers
                                                                                                                                                  AX039517 98 bp
Sequence 9 from Patent WO0063374.
AX039517
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                                        1246 CGGGAGCTGGAGCGCCAGCGAGG 1270
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BD270476.1 GI:33080244
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Best Local Similarity 68.2%;
Matches 58; Conservative (
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PC A61P17
PC A61P3E
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BD270476
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A61P37/06,A61P37/08,C07K14/705,C12N1/15,C12N1/19,C12N1/21, PC
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                                                                                                                                                                                            9908818.9
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    /organism='Artificial Sequence'

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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             1.1%; Score 41.8; DB 6; Length 98; larity 68.2%; Pred. No. 2e+02; Conservative 0; Mismatches 27; Indels
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A method of altering the properties of a membra
in by substitution of the transmembrane domain
Patent: WO 0063373-A 9 26-OCT-2000;
CELLTECH THERAPEUTICS LIMITED (GB)
LOCATION/Qualifiers
                                                  Synthetic transmembrane components
Patent: JP 2002541845-A 9 10-DEC-2002;
CELLTECH THERAPEUTICS LTD
OS Artificial Sequence
PN JP 2002541845-A/9
PD 10-DEC-2002
PF 17-APR-2000 JP 2000612453
PR 16-APR-1999 GB 9908816.3,16-APR-1
                                                                                                                                                                                                                                                                                                                                                                                      Location/Qualifiers
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synthetic construct
other sequences; artificial sequences.
  other sequences; artificial sequences.
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                                      lawson, A.D.G. and Finney, H.M.
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                    (bases 1 to 98)
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Best Local Similarity
Matches 58; Conserva
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A61P11/06, PC A61P1; PC A61P2; PC A61P3; PC A61P3; PC C12N5/10, PC C12N1; PH Key FT source FT
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    /organism='Artificial Sequence'.

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1.1%; Score 41.8; DB 6; Length 1
Best Local Similarity 68.2%; Pred. No. 2e+02;
Matches 58; Conservative 0; Mismatches 27; Indele
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CELLTECH THERAPEUTICS LIMITED (GB)
Location/Qualifiers
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1.1%; Score 41.8; DB 6; Length 100;
Best Local Similarity 68.2%; Pred. No. 2e+02;
Matches 58; Conservative 0; Mismatches 27; Indels
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A method of altering the properties of a membra
in by substitution of the transmembrane domain
betant: WO 0063373-A 10 26-OCT-2000;
CELLTECH THERAPEUTICS LIMITED (GB)
                                                                   /organism="synthetic construct"
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Synthetic transmembrane components
Patent: WO 0063374-A 10 26-OCT-2000;
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Sequence 10 from Patent WO0063374..
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Sequence 10 from Patent WO0063373.
AX039309
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                                                                                                                                                                                             A method of altering the properties of a membrane-associated prote in by substitution of the transmembrane domain Patent: WO 0063373.A 11 26-OCT-2000; CELLTECH THERAPEUTICS LIMITED (GB) LOCATION/QUALIFIERS
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                            92 bp
Sequence 11 from Patent W00063373.
AX039310
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Sequence 11 from Patent W00063374.
AX039519
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AGIP37/06, AGIP37/08, C07K14/705, C12N1/15, C12N1/19, C12N1/21, PC
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                                                                                                                                                                                                                                                                                                                          other sequences; artificial sequences.

I (bases 1 to 94)

S Lawson, A.D.G. and Finney, H.M.
S Lawson, A.D.G. and Finney, H.M.
Synthelic transmembrane components

L Patent: JP 2002541845-A 12 10-DEC-2002;
CELLTECH THERAPEUTICS LTD
OS Artificial Sequence
PN JP 2002241845-A/12
PD 10-DEC-2002
PF 17-ARF-2000 JP 2000612453
PR 16-APR-1999 GB 9908816.3
PR 16-APR-1999 GB 9908816.3
PR 16-APR-1999 GB 9908816.9
ALASTAIR DAVID GRIFFITHS LAWSON, HELENE MARGARET FINNEY PC
CCANALY, A.D.
ALASTAIR DAVID AGIRS (00, AGIRS) (00, AGIPS) 
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/organism='Artificial Sequence'
Location/Qualifiers
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A method of altering the proporties of a membrane in by substitution of the transmembrane domain patent: WO 0063373-A 12 26-0CT-2000;
CELLTECH THERAPEUTICS LIMITED (GB)
Location/Qualifiers

1 .94
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71.6%; Pred. No. 4.2e+02;
iive 0; Mismatches 21;
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other sequences; artificial sequences.
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Synthetic transmembrane components.
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Sequence 12 from Patent WO0063373.
AX039311
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Krenz, J.D
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AUTHORS
TITLE
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HCH388053
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                                                                                                                     1 (bases 1 to 78)
Tsuji,S. and Sanpei,K.
Method for diagnosing spinocerebellar ataxia type 2 and primers
                                                                                                     1179 AGAGCGGGAGCGCCAGGAGCAGGAGGCGGCAGCTGGAGCTGGAGAAGCAGCTGGA
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                                                     Length 94;
                                                  Score 40.4; DB 6; Length 9. Pred. No. 4.2e+02; 0; Mismatches 21; Indels
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synthetic construct
other sequences; artificial sequences.
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Patent: WO 0063374-A 12 26-OCT-2000;
CELLTECH THERAPEUTICS LIMITED (GB)
Location/Qualifiers
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Sequence 12 from patent US 6251589.
AR159552
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Location/Qualifiers
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1 Similarity 71.6%;
53; Conservative
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                                                  Query Match
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AR159552
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FEATURES
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Hyla chrysoscelis DNA for simple sequence repeat (SSR), isolate
                                                                                                        1192 CAGGAGCAGGAGGCCAAGCGGCAGCTGGAGAAGCAGCTGGAGAAGCAGCAGCAGGAGA 1251
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                repetitive DNA.
Hyla chrysoscelis (southern gray treefrog)
Hyla chrysoscelis
Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Buteleostomi;
Amphibia; Batrachia; Anura; Neobatrachia; Hyloidea;
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Isolation and characterization of simple sequence repeat loci in
the gray tree frog, Hyla chrysoscelis
Unpublished
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Score 38; DB 6; I
Pred. No. 1.4e+03;
0; Mismatches 25;
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  Query Match
Best Local Similarity 67.9%;
Matches 53; Conservative
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Run on:

April 28, 2005, 05:12:48; Search time 1763.82 Seconds (without alignments) 12223.299 Million cell updates/sec

US-09-674-237B-2 3642 Title: Perfect

score:

1 atggetcagtttcccacacc......tggaccccagccagcaatga 3642 Sequence:

IDENTITY NUC Gapop 10.0 , Gapext 1.0 Scoring table:

4390206 segs, 2959870667 residues Searched:

4530610 Total number of hits satisfying chosen parameters:

seq length: 0 seq length: 100 Minimum DB 8 Maximum DB 8 Post-processing: Minimum Match 08
Maximum Match 1008
Listing first 45 summaries

Geneseq 16Dec04:\* Database

genesegn1980s:\* genesegn1990s:\*

geneseqn2001bs:\* geneseqn2002bs: geneseqn2000s:\* geneseqn2001as: geneseqn2002as:

genesegn2004as:\* genesegn2004bs:\* geneseqn2003ds:\*

geneseqn2003cs:\*

geneseqn2003as:\* geneseqn2003bs:\* Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

	Description	Adp49483 Oligonucl	Abn38018 Human spl	Adc16446 Short int	Adc16445 Short int	Aac65404 Oligonucl	Aac65405 Oligonucl		Aac65406 Oligonucl	Aac65407 Oligonucl	Acd94308 Human col	Aav68382 Clone #8	Aav17232 SCA2 gene	Aav17233 SCA2 gene	Ads31430 Human gen	Aac65409 Oligonucl	Aad30431 29 mer ol	Aav17231 SCA2 gene	Aac65408 Oligonucl	Aav17230 SCA2 gene	Aai26445 Probe #16
SUMMARIES	ID	ADP49483	ABN38018	ADC16446	ADC16445	AAC65404	AAC65405	ABK89299	AAC65406	AAC65407	ACD94308	AAV68382	AAV17232	AAV17233	ADS31430	AAC65409	AAD30431	AAV17231	AAC65408	AAV17230	AAI26445
	DB	12	ø	10	10	4	4,	9	4	4	10	7	7	0	7	4	9	7	4	7	4
	Query Match Length DB	80	9	81	81	98	100	75	92	94	97	8	78	78	69	88	87	78	86	75	93
ф	Query Match	2.2	1.3	1.2	1.2	1.1	1.1	1.1	1.1	1.1	1.1	1.1	1.0	1.0	1.0	1.0	1.0	1.0	1.0	6.0	6.0
	Score	80	48.8	42.8	42.8	41.8	41.8	41	40.4	40.4	39.2	39	38	38	37.6	37	36.6	36.4	35.8	34	33.4
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Aba74544 Human foe	Aai55023 Probe #23	Aba39360 Probe #17	Aak49188 Human bon	Aak23011 Human bra	Abs48832 Human liv	Abs22756 Human gen	Aat78908 Poly-glut	Aav17234 SCA2 gene	œ	Ads31429 Human gen	Aac65410 Oligonucl	Aac65411 Oligonucl	Adr00028 KRT19 PCR	Adh58952 Silk prot	Ach84145 Human gen	Aav27572 Nucleotid	Adg95147 Synthetic	Abv89298 Human POS	Aai84741 Human pol	Aac10510 Human sec	Ach89027 Human gen	Aax88107 Antifreez	Aax88106 Synthetic	Adh58951 Silk prot
ABA74544	AA155023	ABA39360	AAK49188	AAK23011	ABS48832	ABS22756	AAT78908	AAV17234	ADQ95148	ADS31429	AAC65410	AAC65411	ADR00028	ADH58952	ACH84145	AAV27572	ADQ95147	ABV89298	AAI84741	AAC10510	ACH89027	AAX88107	AAX88106	ADH58951
4	4	4	4	4	4	9	7	~	13	7	4	4	13	12	12	~	13	9	4	m	12	~	~	15
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6.0	6.0	6.0	6.0	6.0	6.0	6.0	6.0	6.0	6.0	6.0	6.0	6.0	6.0	6.0	8.0	9.0	8.0	8.0	8.0	8.0	8.0	8.0	8.0	0.8
33.4	33.4	33.4	33.4	33.4	33.4	33.4	33	33	32.4	32.2	31.4	31.4	31.2	31	30.8	30.6	30.4	30.4	30.4	30	29.8	29.4	29.4	29.4
21	22	23	24	25	26	27	28	59	30	31	32	33	34	35	36	37	38	39	40	41	42	43	44	45
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## ALIGNMENTS

RESULT 1

orthologue; homology; expression distribution; Oligonucleotide array related rat oligonucleotide probe No 99. oligonucleotide array, orthologue, homol change, gene-expression, rat, probe, ss. ADP49483 standard; DNA; 80 BP. 14-JUN-2002; 2002JP-00174208. 14-JUN-2002; 2002JP-00174208. (first entry) (HITA ) HITACHI LTD. WPI; 2004-113862/12. Rattus norvegicus. JP2004016070-A. 22-JAN-2004. 12-AUG-2004 ADP49483; ADP49483 

Oligonucleotide array, useful for measuring ortholog gene-expression distribution, comprising number of oligonucleotides derived from ortholog gene of different organism immobilized on support.

Disclosure; Page 16; 56pp; Japanese.

The invention relates to a novel oligonucleotide array comprising a number of oligonucleotides derived from an orthologue gene of a different organism or species immobilised on a support body. The oligonucleotide array has two sides comprising a gene derived from two different organisms, in which one side comprises a human gene. In the oligonucleotide array a base sequence differs in a different position on the support body. Each of the oligonucleotides is a partial sequence of the orthologue gene of the organism A and organism B. The sequence match degree of the organism species A and the organism species B is less than 10%. The sequence homology of the genes other than the orthologue gene of

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temperature of the variant genes other than the orthologue gene of the organism species B is 20 degrees C or more. The oligonuclectide array is useful for measuring expression distribution of the orthologue gene in different organisms. The method is useful for comparing expression change of the orthologue gene with respect to comparing expression change of the orthologue gene with respect to the orthologue gene in different organisms. The oligonuclectide array has the ability to perform a measurement of gene-expression distribution of two or more types of organism simultaneously. The oligonuclectide array improves reliability of measurement. This polynuclectide sequence represents a probe of a rat gene for comparison against a human gene used
the organism species A and the organism species B is the level-of-statistical-significance value, calculated using the homology searching algorithm: basic local alignment search tool (BLAST) and the value is 0.1 or more. The found value or the calculated value of the melting-
                                                                                                                                                                                                                                                                                                                                                                                                                                                                             the oligonucleotide array of the invention.
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Sequence 80 BP; 19 A; 15 C; 25 G; 21 T; 0 U; 0 Other;

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2876
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                                    Gaps
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 Length 80;
                   0; Indels
2.2%; Score 80; DB 12; I
100.0%; Pred. No. 4.9e-09;
iive 0; Mismatches 0;
                                                                         2877 GAAACTCATTTCAGGGCCCG 2896
                                                                                  GAPACTCATTTCAGGGCCCG 80
                    80; Conservative
           Local Similarity
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Human spliced transcript detection oligonucleotide SEQ ID NO:10766 ABN38018 standard; DNA; 60 BP (first entry) Homo sapiens 15-JUL-2002 ABN38018; ABN38018
ABN38018
ARABN38018
ARAB

Human, mouse, rat, splice transcript, detection, RNA transcript, splice variant, transcriptome, oligonucleotide library, ss.

WO200210449-A2

07-FEB-2002.

20-JUL-2001; 2001WO-IB001903.

28-JUL-2000; 2000US-0221607P. 02-MAY-2001; 2001US-0287724P.

(COMP-) COMPUGEN INC

Mintz L, Mintz E, Shoshan A, Wasserman A,

Faigler

WPI; 2002-257383/30.

Ø New oligonucleotide libraries comprising oligonucleotides which selectively hybridize to mRNAs transcribed from a transcription unit of genome, useful for detecting tissue-, pathology-, and developmentalspecific genes

Example 1; SEQ ID NO 10766; 47pp; English.

The present invention describes oligonucleotide libraries for detecting messenger RNAs that populate a (sub-)transcriptome, where the (sub-)transcriptome comprises messenger RNAs transcribed from multiple transcription units that populate a genome. The library comprises several

The present invention describes an RNA (I) used for the interference or

Claim 71; SEQ ID NO 171; 176pp; English.

of a target gene

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cc oligonucleotides, each capable of hybridising selectively to a set of messenger RNAs transcribed from a given transcription unit of the genome, which encodes one or more messenger RNAs splice variants. The oligonucleotide libraries are useful for detecting mRNAs from a cc oligonucleotide libraries are useful for detecting mRNAs from a cc piological sample, in expression profilling studies, in qualitatively or caracterising the corresponding transcriptome, and in detecting RNA transcripts and splice variants of human or animal cranscriptomes. The libraries may also be used as specialised minical transcriptomes. The libraries may also be used as specialised minical prological or pathological state, and so allowing the detection of tissue companient or pathological state, and so allowing the detection of tissue and pathology-specific pathological condition; to detect conduction; to detect developmental specific genes; and to detect RNA transcripts and splice variants of a transcriptome of a patient suffering from a particular clisor disorder. ABN27253 to ABN59589 represent oligonucleotide sequences from crats, humans and mice, which are used in the exemplification of the present invention. N.B. The sequence data for this patent did not form all the properties of the print of the print
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         9
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              Gaps
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      Short interfering double-stranded RNA oligonucleotide SEQ ID NO:171.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    expression interference; expression inhibition; target gene; short interfering double stranded RNA; cytostatic; gene therapy; proliferative disease; cancer; ds.
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       length of 0-nucleotide to 5-nucleotides on each strand, useful genetic and/or therapeutic tools for interfering or inhibiting
                                                                                                                                                                                                                                                                                                                                                                                                                                                                              directly from WIPO at ftp.wipo.int/pub/published_pct_sequences
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       6; Length 60;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   Caplen NJ, Morgan RA, Fire A, Parrish S, Mousses S;
Kallioniemi O, Cornelison JR, Alton EW, Griesenbach U;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        Indels
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  Sequence 60 BP; 19 A; 17 C; 13 G; 11 T; 0 U; 0 Other;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     1.3%; Score 48.8; DB
88.3%; Pred. No. 0.13;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           0; Mismatches
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IMPERIAL COLLEGE INNOVATIONS LTD
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       (USSH ) US DEPT HEALTH & HUMAN SERVICES.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             В.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           30-JUL-2002; 2002WO-US024226.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            30-JUL-2001; 2001US-0308640P
08-APR-2002; 2002US-0370970P
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          ADC16446 standard; RNA; 81
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             (first entry)
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        Matches 53; Conservative
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   WPI; 2003-248169/24.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          Query Match
Best Local Similarity
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        WO2003012052-A2.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                18-DEC-2003
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             ADC16446;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          (IMCO-)
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ADC16446/c
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inhibition of expression of a target gene, where (I) comprises double stranded RNA of 15-40 nucleotides in length and a 3' or 5' overhang having a length of 0-inucleotide to 5-incleotides on each strand, where the sequence of the double stranded RNA is substantially identical to a portion of a mRNA or transcript of the target gene. Also described: (1) interfering with or inhibiting the expression of a target gene in a cell by exposing the cell to an amount of (I); (2) a gene silencing array comprising a substantially flat substrate, and addressably arrayed different double-stranded RNAs; (3) an array-based method of assessing a phenotypic effect of a double-stranded RNA on a target gene; (4) validating a gene as a potential drug target for a disease or condition; (5) selecting an optimised sequence of a double-stranded RNA for interference with or inhibition of expression of a target gene in a cell; and (6) a short double-stranded RNA effective for interfering with or inhibiting expression of a target gene comprising any of 311 20-78 cucleotide sequences (see ADC16276 to ADC16586). (I) has cytostatic activity, and can be used in gene therapy. The RNAs are useful as reverse genetic and/or therapeutic tools for interfering or inhibiting expression of a target gene. They are useful for interfering or inhibiting expression
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     e.g. cancer
             $$$$$$$$$$$$$$$$$$$$$$$$$$$$
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1187 AGCGCCAGGAGCAGGAGGCCAAGCGGCAGCTGGAGCTGGAGAAGCAGCTGGAGAAGCAGC 1246
                                                                                                                     21
                                                                                                            Gaps
                                                            ;
0
                           1.2%; Score 42.8; DB 10; Length 81;
11.8%; Pred. No. 3.9;
ve 0; Mismatches 22; Indels (
Sequence 81 BP; 0 A; 27 C; 27 G; 0 T; 27 U; 0 Other;
                                                                                                                                                     1247 GGGAGCTGGAGCGGCAGC 1264
                                                                                                                                                                        20 AGCAGCAGCAGCAGC 3
                                       Local Similarity 71.8%;
                                                          56; Conservative
                                                                                                                       80
                              Query Match
                                                            Matches
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Short interfering double-stranded RNA oligonucleotide SEQ ID NO:170.
                                                                                                                     ADC16445 standard; RNA; 81 BP
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                                                                                                                                                                                                                    ADC16445;
RESULT 4
ADC16445
                                                                                                                     THE STANDARD STANDARD
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expression interference; expression inhibition; target gene; short interfering double stranded RNA; cytostatic; gene therapy; proliferative disease; cancer; ds.

WO2003012052-A2. Synthetic.

13-FEB-2003

30-JUL-2002; 2002WO-US024226.

30-JUL-2001; 2001US-0308640P. 08-APR-2002; 2002US-0370970P.

(USSH ) US DEPT HEALTH & HUMAN SERVICES. (CARN-) CARNEGIE INST WASHINGTON. (IMCO-) IMPERIAL COLLEGE INNOVATIONS LTD.

Caplen NJ, Morgan RA, Fire A, Parrish S, Mousses S; Kallioniemi O, Cornelison JR, Alton EW, Griesenbach U;

WPI; 2003-248169/24.

New RNA comprising double stranded RNA and a 3' or 5' overhang having a length of 0-nucleotide to 5-nucleotides on each strand, useful as reverse genetic and/or therapeutic tools for interfering or inhibiting expression

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The present invention describes an RNA (I) used for the interference or inhibition of expression of a target gene, where (I) comprises double stranded RNA of 15-40 nucleotides in length and a 3' or 5' overhang having a length of 0-nucleotides in length and a 3' or 5' overhang. Invention of a mand of 15-40 nucleotides on each strand, where the sequence of the double stranded RNA is substantially identical to a portion of a mand of the expression of a target gene in a cell interfering with or inhibiting the expression of a target gene in a cell of the expression of a target gene in a cell or expression of a target gene in a cell or expression of a target gene in a cell or expression of a target gene in a cell or expression of a double-stranded RNA or a target gene; (4) and target gene or condition; (5) selecting an optimised sequence of a double-stranded RNA for and (6) a short double-stranded RNA expression of a target gene in a cell; and (6) a short double-stranded RNA effective for interfering with or inhibiting expression of a target gene condition; and (6) a short double-stranded RNA effective for interfering with or inhibiting expression of a target gene condition; and (6) a short double-stranded RNA effective for interfering with or inhibiting expression of a target gene condition; and (6) a short double-stranded RNA effective for interfering with or inhibiting expression of a target gene condition; and (6) a short double-stranded RNA effective for interfering with or inhibiting expression of a target gene condition; and expression of a target gene condition; of a target gene. They are useful for treating proliferative diseases,
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      1187 AGCGCCAGGAGCAGGAGGCCAAGCGGCAGCTGGAGCAGAAGCAGCTGGAGAAGCAGC 1246
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              Gaps
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          Membrane-associated protein; antiviral; antibacterial; antiparasitic;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          immunomodulatory; anticancer; antinflammatory; antiasthmatic;
antidiabetic; neuroprotective; chimeric receptor; infection;
inflammatory disorder; autoimmune disorder; cancer; allergy; asthma;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        ;
0
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              DB 10; Length 81;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               Oligonucleotide B6463 for chimeric receptor construction.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             eczema; cystic fibrosis; sickle cell anaemia; psoriasis; multiple sclerosis; organ transplant rejection; diabetes; transmembrane domain; ss.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      Indels
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              Sequence 81 BP; 27 A; 27 C; 27 G; 0 T; 0 U; 0 Other;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        22;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         Match 1.2%; Score 42.8; DE Local Similarity 71.8%; Pred. No. 3.9; es 56; Conservative 0; Mismatches
                                             Claim 71; SEQ ID NO 170; 176pp; English.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           CLLT ) CELLTECH THERAPEUTICS LTD
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        62 AGCAGCAGCAGCAGC 79
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            BP.
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           1247 GGGAGCTGGAGCGGCAGC
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        AAC65404 standard; DNA; 98
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                14-FEB-2001 (first entry)
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  of a target gene.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           WO200063373-A1.
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     AAC65404;
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        Matches
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of membrane-associated

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The present sequence was used in the construction of chimeric receptors.

The properties and level of expression of a membrane-associated protein
may be altered by substituting a transmembrane region or a membrane-
anchoring region for transmembrane or membrane-anchoring regions that are
not naturally part of the protein. The relative response of membrane-
associated proteins to cell surface-associated antigen versus antigen in
solution, and the sensitivity of intracellular signaling mediated by
membrane-associated proteins can be altered. They can be important in
treatment of, e.g. HIV infection, bacterial infections, parasitic
infections, inflammatory/autoimmune disorders (e.g. relumatoid arthritis,
osteoarthritis or inflammatory bowel disease), cancer, allergic/atopic
diseases (e.g. asthma or eczema), congenital disorders (e.g. cystic
fibrosis or sickle cell anaemia), dermatological disorders (e.g.
psoriasis), neurological disorders (e.g. multiple sclerosis), organ
transplant rejection, graft-versus-host diseases, or metabolic/idiopathic
diseases (e.g. diabetes)
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 1186 GAGCGCCAGGAGCAGGAGGCCAAGCGGCAGCTGGAGCAGCAGCAGCTGGAGGAAGCAG 1245
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              Membrane-associated protein; antiviral; antibacterial; antiparasitic; immunomodulatory; anticancer; antiinflammatory; antiasthmatic; antidiabetic; neuroprotective; chimeric receptor; infection; inflammatory disorder; autoimmune disorder; cancer; allergy; asthma; eczema; cystic fibrosis; sickle cell anaemia; psoriasis; multiple sclerogis; organ transplant rejection; diabetes;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     Altering the properties or level of expression of membrane-associate proteins, e.g., to change responses to cell surface antigens or the sensitivity of intracellular signaling.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             Oligonucleotide B6464 for chimeric receptor construction.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  Sequence 98 BP; 2.A; 37 C; 25 G; 34 T; 0 U; 0 Other;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               1246 CGGGAGCTGGAGCGCCAGCGAGAGG 1270
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             CAGCAGGAGCAGCACCCAAAAG 4
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       (CLLT ) CELLTECH THERAPEUTICS LTD.
                                                                                                                Example 2; Fig 3; 47pp; English.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              AAC65405 standard; DNA; 100 BP.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  99GB-00008816,
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            17-APR-2000; 2000WO-GB001471
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          68.2%;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             (first entry)
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                58; Conservative
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           transmembrane domain; ss
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             Finney HM, Lawson ADG;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 WPI; 2001-015774/02.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          Query Match
Best Local Similarity
Matches 58; Conserva
WPI; 2001-015774/02
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   WO200063373-A1
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  16-APR-1999;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          26-OCT-2000.
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               Synthetic
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           88
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      28
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         AAC65405;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            RESULT 6
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1186 GAGCGCCAGGAGGCAGGCCAAGCGGCAGCTGGAGCAGAAGCAGCTGGAGAAGCAG 1245 anchoring region for transmembrane or membrane-anchoring regions that are anchoring region for transmembrane or membrane-anchoring regions that are not naturally part of the protein. The relative response of membrane-associated proteins to cell surface-associated antigen versus antigen in solution, and the sensitivity of intracellular signaling mediated by membrane-associated proteins can be altered. They can be important in treatment of e.g. HIV infection, bacterial infections, parasitic infections, inflammatory/autoimmune disorders (e.g. rheumatoid arthritis, osteoarthritis or inflammatory bowel disease), cancer, allergic/atopic diseases (e.g. asthma or eczema), congenital disorders (e.g. cystic fibrosis or sickle cell anaemia), dermatological disorders (e.g. cystic fibrosis), neurological disorders (e.g. multiple sclerosis), organ psoriasis), neurological disorders (e.g. multiple sclerosis), organ transplant rejection, graft-versus-host diseases, or metabolic/idiopathic diseases (e.g. diabetes) The present sequence was used in the construction of chimeric receptors. The properties and level of expression of a membrane-associated protein may be altered by substituting a transmembrane region or a membrane-Altering the properties or level of expression of membrane-associated proteins, e.g., to change responses to cell surface antigens or the sensitivity of intracellular signaling. Human; trinucleotide repeat instability; TNR; cancer; ds; fragile X syndrome; Huntington's disease; myotonic dystrophy; spinal and bulbar muscular atrophy; SBMA; SCA I; Kennedy's disease; spinocerebellar ataxia type I; Friedreich's ataxia; DRPLA; Gentatorubaral-palidoluyahan atrophy; SCA8; SCA12; SCA2; SCA6; SCA7; SCA3; Machado-Joseph disease; testicular cancer; prostate cancer. 0; Gaps DB 4; Length 100; 27; Indels Sequence 100 BP; 34 A; 26 C; 38 G; 2 T; 0 U; 0 Other; Score 41.8; DB Fred. No. 7.5; 0; Mismatches 1246 CGGGAGCTGGAGCGCCAGCGAGAGG 1270 CAGCAGGAGCAGCACCCAAAAG 99 Example 2; Fig 3; 47pp; English 20-DEC-2001; 2001WO-US049800. 21-DEC-2000; 2000US-00742025. Local Similarity 68.2%; tes 58; Conservative Trinucleotide repeat CAG25. ABK89299 standard; DNA; 75 (first entry) (UYNE-) UNIV NEBRASKA WO200257494-A1. Homo sapiens 21-OCT-2002 25-JUL-2002. ABK89299; Query Match Matches RESULT 7 **ABK**89299 ઠે 임 à

Gaps

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Score 41.8; DB 4; Length 98; Pred. No. 7.4; 0; Mismatches 27; Indels

Detecting alterations in trinucleotide repeat (TNR) tract lengths in

Miret JJ;

Lahue RS, Pelletier R,

WPI; 2002-575460/61

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The invention relates to detecting (MI) alterations in trinucleotide repeat (TMR) tract lengths comprising: (i) contacting mammalian cells with a shuttle vector (containing approximately 25 repeats) that enters and replicates in the cells, (ii) recovering the replicated shuttle vector from the cells, (ii) introducing the vector into a yeast cell in the presence of a selection agent or (where the expanded TMR confers a Hist-phenotype) in the absence of histidine, alteration to the TMR tract confers resistance to the selective agent or Hist-phenotype; and (iv) selecting yeast cells with the shuttle vector containing TMR tract confers resistance to the selective agent or Hist-phenotype; and (iv) selecting yeast cells with the shuttle vector containing TMR tract confers resistance to the selective agent. Also included is an adaptation of the vest cells in the absence of uracil. The methods of the present invention are useful for identifying disorders with genetic alterations associated with TMR instability such as cancer (e.g. testicular and prostate), Fragile x syndrome, Huntington's disease, myotonic dystrophy, spinal and bulbar muscular atrophy (SBMA), priedreich's ataxia and kennedy's disease. The present sequence is the CAG32 TMR known to be unstable in Human sperm and in yeast which was tested in the method
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       1192 CAGGAGCAGGAGGCCAAGCGGCAGCTGGAGCTGGAGAAGCAGCTGGAGAAGCAGCGGGAG 1251
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               mammalian cells useful for identifying disorders associated with TNR instability such as cancer, Fragile X syndrome, Huntington's disease or
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        Membrane-associated protein; antiviral; antibacterial; antiparasitic;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                0; Gaps
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            immunomodulatory; anticancer; antiinflammatory; antiaethmatic;
antidiabetic; neuroprotective; chimeric receptor; infection;
inflammatory disorder; autoimmune disorder; cancer; allergy; asthma;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   Score 41; DB 6; Length 75;
Pred. No. 10;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            0; Mismatches 20; Indels
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 Oligonucleotide B6465 for chimeric receptor construction.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             eczema; cystic fibrosis; sickle cell anaemia; psoriasis;
multiple sclerosis; organ transplant rejection; diabetes;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              Sequence 75 BP; 25 A; 25 C; 25 G; 0 T; 0 U; 0 Other;
                                                                                  Example 1; Page 24; 43pp; English.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          (CLLT ) CELLTECH THERAPEUTICS LTD
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 to be unstable in Human sperm a
of the invention for expansion
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       AAC65406 standard; DNA; 92 BP
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   99GB-00008816.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   1.1%;
Local Similarity 72.6%;
les 53; Conservative (
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       17-APR-2000; 2000WO-GB001471
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        CTGGAGCGGCAGC 1264
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        (first entry)
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 CAGCAGCAGCAGC 73
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      transmembrane domain; ss
                                           myotonic dystrophy.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     40200063373-A1
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        14-FEB-2001
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                26-0CT-2000
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        1252
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 AAC65406;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     Query Match
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                Matches
  원
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The properties and level of expression of a membrane-associated protein may be altered by substituting a transmembrane region or a membrane and notaring region for transmembrane or membrane-anchoring regions that are not naturally part of the protein. The relative response of membrane sasociated proteins to cell surface-associated antigen versus antigen in colution, and the sensitivity of intracellular signaling mediated by solution, and the sensitivity of intracellular signaling mediated by conting the cell surface-associated proteins can be altered. They can be important in treatment of, e.g. HIV infection, bacterial infections, parasitic infections, inflammatory/autoimmune disorders (e.g. rheumatoid arthritis, osteoarthritis or inflammatory bowel disease), cancer, allergic/atopic diseases (e.g. asthma or eczema), congenital disorders (e.g. cystic fibrosis or sickle cell anaemia), dermatological disorders (e.g. cystic fibrosis or sickle cell anaemia), dermatological disorders (e.g. metabolic/idiopathic riseases (e.g. diseases (e.g. metabolic/idiopathic diseases (e.g. diseases (e.g. diseases (e.g. diseases (e.g. metabolic/idiopathic diseases (e.g. diseases (e.g. metabolic/idiopathic diseases (e.g. 
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 1179 AGAGCGGGAGCGCCAGGAGCAGGGCCAAGCGGCAGCTGGAGCTGGAGAAGCAGCTGGA 1238
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       ö
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     27
                                                                                                                                                                                                                                                                                            The present sequence was used in the construction of chimeric receptors
                                                                                                              Altering the properties or level of expression of membrane-associated proteins, e.g., to change responses to cell surface antigens or the sensitivity of intracellular signaling.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     86 AGAACAGGAGCAGCAGCAGTAGCAGGAGCAGCAGCAGGAGCAGCAGGAGCAGGAGCA
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        Membrane-associated protein, antiviral, antibacterial; antiparasitic; immunomodulatory, anticancer; antiinflammatory; antiasthmatic; antidiabetic; neuroprotective; chimeric receptor; infection; inflammatory disorder; autoimmentory disorder; autoimmentory disorder; autoimmentory and order; autoimmentory and order; autoimmentory allergy; asthma; eccema; oystic fibrosis; alckie cell anaemia; psoriasis; multiple sclerosis; organ transplant rejection; diabetes;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       0; Gaps
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             DB 4; Length 92;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       Oligonucleotide B6466 for chimeric receptor construction.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       Indels
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   Sequence 92 BP; 2 A; 34 C; 24 G; 32 T; 0 U; 0 Other;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       21;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       Local Similarity 71.6%; Pred. No. 16; les 53; Conservative 0; Mismarana.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    (CLLT ) CELLTECH THERAPEUTICS LTD.
                                                                                                                                                                                                                                     Example 2; Fig 3; 47pp; English
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         AAC65407 standard; DNA; 94 BP.
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  1239 GAAGCAGCGGGAGC 1252
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            GCAGGAGCAGCAGC 13
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             14-FEB-2001 (first entry)
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             transmembrane domain; ss
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     diseases (e.g. diabetes)
   Lawson ADG;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 Finney HM, Lawson ADG;
                                                          WPI; 2001-015774/02.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 WO200063373-A1
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Finney HM,
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       Synthetic
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   AAC65407;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                Query Match
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 Matches
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WPI; 2003-182626/18.

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The properties and level of expression of a membrane-associated protein may be altered by substituting a transmembrane region or a membrane-anchoring region for transmembrane or membrane-anchoring region for transmembrane or membrane-associated proteins to cell surface-associated antigen versus antigen in solution, and the sensitivity of intracellular signaling mediated by membrane-associated proteins can be altered. They can be important in treatment of, e.g. HIV infection, bacterial infections, parasitic infections, inflammatory/autoimmune disorders (e.g. rheumatoid arthritis,
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          infections, inflammatory/autoimmune disorders (e.g. rheumatoid arthritis, obsteoarthritis or inflammatory bowel disease), cancer, allergic/atopic diseases (e.g. asthma or eczema), congenital disorders (e.g. cystic fibrosis or sickle cell anaemia), dermatological disorders (e.g. cystic transplant rejection, graft-versus-host diseases), ocusion, graft-versus-host diseases, or metabolic/idiopathic diseases (e.g. diabetes)
                                                                                                                                                                                                                                          present sequence was used in the construction of chimeric receptors.
                                                                         Altering the properties or level of expression of membrane-associate proteins, e.g., to change responses to cell surface antigens or the sensitivity of intracellular signaling.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             Sequence 94 BP; 32 A; 25 C; 35 G; 2 T; 0 U; 0 Other;
                                                                                                                                                                                          Example 2; Fig 3; 47pp; English
                         WPI; 2001-015774/02
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1179 AGAGCGGGAGCGCCAGGAGCAGGAGCCCAAGCGGCAGCTGGAGCTGGAGCAGCTGGA 1238
                                                               0; Gaps
Score 40.4; DB 4; Length 94;
Pred. No. 16;
0; Mismatches 21; Indels
                                                                                                GAAGCAGCGGGAGC 1252
          .1 Similarity 71.6%;
53; Conservative
                                                                                                                       84
                                                                                                                       GCAGGAGCAGCAGC
 Query Match
Best Local S
                                                                                                                       7
                                                                                                1239
                         Matches
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Human colon cancer cell expressed cDNA #2720.
   ACD94308 standard; cDNA; 97 BP.
                  (first entry)
                                                             Homo sapiens.
                  23-SEP-2003
           ACD94308;
                                                     gene; ss.
ACD94308/
```

breast cancer; population genome analysis; genetic shift; cancer; antibiotic resistence; antibiotic non-tolerance; congenital disease; agriculture; food crop genome; resistance gene; retrovirus; influenza virus; eukaryotic pathogen detection; trypanosome; Plasmodium; Open reading frame detection; genome sequencing; colon cancer;

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99US-00406117.
                                                                                  98US-00196716.
                                                                                                             SIMPSON A J G.
US2002155438-A1.
                                                      27-SEP-1999;
                                                                                  20-NOV-1998;
                          24-OCT-2002.
                                                                                                             (SIMP/)
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Brentani RR;

Simpson AJG, Neto ED,

NETO E D. BRENTANI R'R.

(NETO/) (BREN/)

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The invention describes a method of determining open reading frames in the genome of organism, comprising contacting mRNA from cell of organism with a single oligonucleotide primer (I) at low stringency, preparing single-stranded coDNA by reverse transcribing mRNA with (I), amplifying single-stranded cDNA by reverse transcribing mRNA with (I), amplifying single-stranded cDNA by reverse transcribing mRNA with (I), amplifying connected by the method is useful for: determining that a known manier connected sequence from a genome of an organism corresponds to a nucleotide sequence from a genome of an organism corresponds to a nucleotide sequence from a genome of an organism corresponds to a long connect of an open reading frame; for preparing a contig, mucleic acid molecule from a genome of an organism. mRNA is obtained from mammalian corresponds to a subject and can be used to carry out genetic analyses of all or part of subjects and can be used to carry out genetic analyses of large or small populations. further, it can be used to study living systems to determine if, e.g. there have been genetic shifts which render an individual or population more or less likely to be afflicted with diseases such as cancer, to determine antibiotic resistance or non-tolerance, and so forth. The method can also be used to offspring through ova or sperm. The analyses for pathological conditions can be trucied out in all animals, plants, birds, fish, etc. Using this method, in the area of agriculture, for example the genomes of food crops can be cut in the area of agriculture, for example the genomes of food crops can be cut and so be studied in this way. Similarly, the method permits determination of the pathogens which integrate into the genome, such as retroviruses and other integrating viruses such as influence are processed the method is also applied to eukaryotic pathogenes. The method is also applied to eukaryotic pathogenes with a such connected to the entail of the ent
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               1196 AGCAGGAGGCCAAGCGGCAGCTGGAGCAGCAGCTGGAGAAGCAGCAGCAGCGGAGGTGG 1255
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                trypanosomes, different types of Plasmodium, etc. The method essentially eliminates sequencing of non-coding portions. This sequence represents a polynucleotide isolated from human colon cancer cell cDNA library
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                Determining open reading frames of genome of an organism e.g. a human suffering from cancer involves use of single oligonucleotide primer at low stringency for preparing single-stranded cDNA from mRNA of
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            0; Gaps
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 nucleic acid analysis, variation assessment, neurological disease;
Huntington's chorea, PCR suppression, ss.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              1.1%; Score 39.2; DB 10; Length 97; 33.4%; Pred. No. 31; v.e 0; Mismatches 34; Indels 0
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        Clone #8 fragment identified by CAG repeat analysis method
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           repeat; human; genome analysis; medical diagnostic;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           Sequence 97 BP; 0 A; 39 C; 0 G; 57 T; 0 U; 1 Other;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   1256 AGCGGCAGCGAGAGGAGGAGGAGGAGGAGA 1288
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      AGAAGAAGAAGAAGAAGAAGAAGAAGAAGA
                                                                                                                                                                                                      Example 9; Page 407; 959pp; English
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       AAV68382 standard; DNA; 89 BP.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    Local Similarity 63.4%;
es 59; Conservative
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          (first entry)
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                                                                                                                                                   individual
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ID AAV68
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o'

Smith CL;

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1192 CAGGAGCAGGAGGCCAAGCGGCAGCTGGAGAAGCAGCTGGAGAAGCAGCAGCAGGAG 1251

    by PCR and determining number

                                                                                                                                                                                                                                                                                                                                                              This sequence represents a fragment of the SCA2 gene. It can be used in the method of the invention for diagnosing spinocerebellar ataxis type II. by performing PCR on the test DNA using two primers hybridising to parts of the SCA2 gene sequence, and determining the number of CAG repeats in the amplified products. The method provides an easy means for the diagnosis of spinocerebellar ataxis type II
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          SCA2 gene; spinocerebellar ataxis type II; CAG repeat; PCR primer; ss.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    DB 2; Length 78;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            Sequence 78 BP; 23 A; 30 C; 25 G; 0 T; 0 U; 0 Other;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     Pred. No. 55;
0; Mismatches
                                                                                                                                                                                                                                                               spinocerebellar ataxis type II
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  Score 38;
Pred. No. 5
                                                                                                                                                                                                                                                                                                                             Disclosure; Page 13; 23pp; Japanese.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  SCA2 gene CAG repeat unit fragment.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                1252 CTGGAGCGCCAGCGAGAG 1269
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         78
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              BP
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 96WO-JP001999.
                                                             96WO-JP001999
                                                                                                   96WO-JP001999
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       67.98;
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          AAV17233 standard; DNA; 78
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          29-JUN-1998 (first entry)
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                Query Match
Best Local Similarity 67.9°
Matches 53; Conservative
                                                                                                                                                                                                                                                                 Diagnosing spinocere
of CAG repeat units
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   WPI; 1998-120796/11.
                                                                                                                                                                                   Sanpei K;
                                                                                                                                                                                                                       WPI; 1998-120796/11
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 Sanpei K;
                                                                                                                                         (SRLS-) SRL INC.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       (SRLS-) SRL INC.
                                                             18-JUL-1996;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 18-JUL-1996;
                                                                                                   18-JUL-1996;
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         WO9803679-A1
                     29-JAN-1998
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   Synthetic.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             Tsuji S,
                                                                                                                                                                                 Tsuji S,
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  AAV17233;
  셤
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   1183 CGGGAGCGCCAGGAGCAGGAGGCCAAGCGGCAGCTGGAGCAGCAGCAGCAGCAGAAG 1242
                                                                                                                                                                                                                                                                                                                                                                                                                                        This sequence represents a fragment of a human CAG repeat containing clone DNA sequence isolated using the method of the invention. The method is for analysing nucleic acids in a sample, and comprises: (a) providing a sample containing nucleic acid, a first oligonucleotide primer comprising a CTG repeat, a second oligonucleotide primer comprising a CAG repeat and a polymerase and PCR reagents; (b) preparing the nucleic acid so that it is amplifiable; (c) amplifying the nucleic acid with the first and second primers; and (d) detecting the amplified product. The method is used to distinguish between the expression of genes in two or more blological samples, e.g. body fluids, cells, solid tissue or solid and differentiate between normal and diseased tissue or to assess the variation within monozygonic twin pairs. The method allows the isolation
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              and analysis of genome subsets containing CAG repeats which are known to be important in a number of neurological diseases including Huntington's chorea. The method uses PCR suppression, in which only fragments which contain a target repeat are efficiently amplified. This allows accurate identification of differentially expressed genes in various cell types. Genome complexity is reduced by the new method which targets genomic subsets containing CAG repeats
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         Analysing nucleic acid samples - using amplification primers which contain CAG or CTG tri:nucleotide repeats for differential display of
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               Gaps
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               ö
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     1.1%; Score 39; DB 2; Length 89; 65.5%; Pred. No. 33;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             30; Indels
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               Sequence 89 BP; 2 A; 23 C; 37 G; 27 T; 0 U; 0 Other;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             0; Mismatches
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   1243 CAGCGGGAGCTGGAGCGCGAGAG 1269
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       caecccaccaecaecaecaecae
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     SCA2 gene CAG repeat unit fragment.
                                                                                                                                                                                                                                                                                                                                                                                                      Example; Page 32; 44pp; English
                                                                                                                                                                                                                                                                                                                                                              samples from different sources.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             AAV17232 standard; DNA; 78 BP.
                                                                                                                    98WO-US008616
                                                                                                                                                          97US-0045078P
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           57; Conservative
                                                                                                                                                                                                                                                                                WPI; 1998-594983/50.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          Best Local Similarity
                                                                                                                                                                                                (UYBO-) UNIV BOSTON
Homo sapiens
                                   WO9849345-A1
                                                                                                                                                          29-APR-1997;
                                                                                                                    29-APR-1998;
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                                                                         05-NOV-1998
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Diagnosing spinocerebellar ataxis type II - by PCR and determining number of CAG repeat units.

SCA2 gene; spinocerebellar ataxis type II; CAG repeat; PCR primer; ss

WO9803679-A1.

Synthetic

BX SX EX BX BX SX B

53

Query Match

Matches

8 셤 ઠે AAV17232;

RESULT 12 AAV17232

Disclosure; Page 13-14; 23pp; Japanese.

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0; Gaps

25; Indels

9

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The invention relates to a mucleic acid hybridisation probe comprising a labelled, single copy nucleic acids of at least 50 nucleotides, which will hybridise to a deduced single copy sequence interval in target nucleic acid (TNA) of known sequence. The single copy sequence is deduced by comparing the target nucleic acid (e.g. a disease causing gene) with a collection of high and low complexity repeat sequences as found in the genome of the organism from containing the target nucleic acid. The probe is generated by PCR on the target sequence. The probe is essentially free of blocking nucleic acid sequences which will hybridise to repeat sequences within the genome of which the TNA is a part, and is labelled with a label selected from fluorochrome-responsive labels, fluorochromes, calorimetric chemical, conjugated proteins, antibodies, antigens and
                                                                                                                                                                                                                                                                                                                                                                                                                                                                              1192 CAGGAGCAGGAGCCCAAGCGGCAGCTGGAGCTGGAGAAGCAGCTGGAGAAGCAGCAGCGGGAG 1251
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        Single copy genomic hybridization probes for detecting specific nucleic acid sequences in sample by in situ hybridization useful for detection of acquired or inherited genetic diseases.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       historical cycle regulation defective, S. cerevisiae homologue A; HIRA; low complexity repeat; in situ hybridisation; Southern bloc; chromosome breakpoint; inherited genetic disease; neoplastic disorder; chromosome 22; Di
This sequence represents a fragment of the SCA2 gene. It can be used in the method of the invention for diagnosing spinocerebellar ataxis type II, by performing PCR on the test DNA using two primers hybridising to parts of the SCA2 gene sequence, and determining the number of CAG repeats in the amplified products. The method provides an easy means for the diagnosis of spinocerebellar ataxis type II
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      9
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       0; Gaps
                                                                                                                                                                                                                                                                                                                              Score 38; DB 2; Length 78;
Pred. No. 55;
0; Mismatches 25; Indels
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    low complexity tandem repeat sequence #17.
                                                                                                                                                                                                                                                                 Sequence 78 BP; 23 A; 30 C; 25 G; 0 T; 0 U; 0 Other;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            Example 1; SEQ ID NO 463; 30pp; English.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 1252 CTGGAGCGCCAGCGAGAG 1269
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      78
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        BP.
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                                                                                                                                                                                                                                                                                                                                                                    Best Local Similarity 67.9%;
Matches 53; Conservative
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      61 cadcadccccccccccc
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        ADS31430 standard; DNA; 69
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                (first entry)
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         (KNOL/) KNOLL J H M.
(ROGA/) ROGAN P K.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           WPI; 2002-062378/08.
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                                                                                                                                                                                                                                                                                                                                             Query Match
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ID ADS3

XX ADS31430

ID B Huma

XX ADS3

XX ADS3

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their mixtures. The probe is useful in a hybridisation method, where the hybridisation method is from in situ hybridisation, Southern blot, and cord conter methods in which nucleic acid is immobilised, where the method further comprises selecting a single copy nucleic acid which will content acid which will a further comprises selecting a single copy nucleic acid which will content and person or triplicon sequence domain. The probe is useful for families in a genome. The method comprises reacting a labelled probe with the genome, causing the probe to hybridise and ascertaining if the probe hybridises to the genome at more than three preferably ten different contermining as a determination of new repeat sequence family, where the determining actomosome breakpoint and is useful in the fields for determining a chromosome breakpoint and is useful in the fields for determining a chromosome breakpoint and is useful in the fields for cytogenetics and molecular genetics for determining the presence of specific nucleic acid sequences in a sample of eukaryotic origin, e.g. the probe may be used to analyse specific chromosomal locations by in situ hybridisation as a detection of acquired or inherited genetic diseases especially for detection of acquired or inherited genetic comprising the human HIRA gene (histone cell cycle regulation defective, comprising the human HIRA gene (histone cell cycle regulation defective, comprising the human HIRA gene (histone cell cycle regulation defective, comprising the human HIRA gene (histone cell cycle regulation defective, comprising the probes of the invention. HIRA is located on threated form and within the human genome used to analyse the HIRA gene for repeat found within the human genome used to analyse the HIRA gene for repeat found within the human genome used to analyse the HIRA gene for repeat regions. Note: The sequence data for this patent did not form parting of the printed specification, but was obtained in electronic promparation.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         ö
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       or the printed specification, but was obtained in electronic format directly from USPTO at seqdata uspto gov/sequence.html?DocID=20030224356.
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  Membrane-associated protein; antiviral; antibacterial; antiparasitic; immunomodulatory; anticancer; antiinflammatory; antiasthmatic; antidiabetic; neuroprotective; chimeric receptor; infection; inflammatory disorder; autoimmune disorder; cancer; allergy; asthma;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         Gaps
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     1.0%; Score 37.6; DB 7; Length 69; 72.1%; Pred. No. 65; ve 0; Mismatches 19; Indels
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              Oligonucleotide B6468 for chimeric receptor construction.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                eczema; cystic fibrosis; sickle cell anaemia; psoriasis; multiple sclerosis; organ transplant rejection; diabetes; transmembrane domain; ss.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             Sequence 69 BP; 23 A; 23 C; 23 G; 0 T; 0 U; 0 Other;
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Thiney HW, Lawson ADG;

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Finney HW, Lawson ADG;

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WPI; 2001-015774/02.

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Altering the properties or level of expression of membrane-associated proteins, e.g., to change responses to cell surface antigens or the properties and level of expression of a membrane-associated protein the properties and level of expression of a membrane-associated protein may be altered by substituting a transmembrane region or a membrane-associated protein companies and level of expression of a membrane-associated protein companies and level of expression of a membrane-associated protein companies or membrane-associated protein companies or membrane-associated by substituting a transmembrane and antigen or a membrane-associated proteins to cell surface-associated antigen were second to the sensitivity of intracellular signaling mediated by membrane-associated proteins coll surface-associated antigen versus antigen in coll surface-associated antigen versus antigen in coll surface by coll surface-associated antigen and the sensitivity of intracellular signaling mediated by membrane-associated proteins coll surface-associated antigen and coll surface-associated antigen in coll surface-associated antigen and coll surface associated and seases (e.g. HV infection, bacterial infections, parasitic cost consentations, inflammatory/autoimmune disorders (e.g. rheumatoid arthritis, osteoarthritis or inflammatory bowel disease), cancer, allergic/atopic consensations in surface coll associated and diseases (e.g. sether cell anaemia), dermatological disorders (e.g. contaction, graft-versus-host diseases, or metabolic/idiopathic contaction, graft-versus-host diseases, or metabolic/idiopathic contactions and con
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1242 GCAGCGGGAGCTGGAGC 1258

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Search completed: April 28, 2005, 08:43:21 Job time : 1764.82 secs THIS PAGE BLANK (USPTO)

Perfect score:

Sequence:

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OM nucleic

Run on:

Scoring table:

Searched:

Minimum DB Maximum DB

Database

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CC199586 94 bp mRNA linear GSS 09-MAY-2003
XE464 BayGenomics Gene Trap Library pGT1Lxf Mus musculus CDNA, mRNA
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CELL_LINE&KEY=XE464
CG572531 OST203191
CD497616 Gm Ckr295
AA726119 vuBBbll.r
CR126087 PCrward s
CG572499 OST203112
AZ476761 1M0295B19
BQ234452 hd45b08.G
CR147383 Reverse s
BQ609943 1030014C1
AI316382 uk60a03.y
CV295497 EST883874
D18610 MUSGS01671
BE662032 bs11e10.y
BQ234381 hd45h04.9
AI947161 bb355907.y
AN674805 AV674805
BG237998 TaE05009F
BG337998 TaE05009F
GG878955 SGP139924
                                                                                                                                                                                                                                                                                                                                                                                                                                 Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Buteleostomi;
Mammalia; Eutheria; Rodentia; Sciurognathi; Muridae; Murinae; Mus.
1 (bases 1 to 94)
                                                                                                                                                                                                                                                                                                                                                                                                                                                                             http://baygenomics.ucsf.edu/
Unpublished (2001)
Contact: BayGenomics
Bay Area Functional Genomics Consortium (BayGenomics)
Email: info@baygenomics.ucsf.edu
Sequence tag generated by 5' RACE of total RNA from gene trap ES
cell line. ES cell lines harboring insertion mutation of target
gene are available upon request from BayGenomics. Annotation
information available from
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    CCTCCAGCAGCAGCAGCTGTGTGTGTGTCAGTCATCAAGGCTGAAATACAGGCAGTTATTC
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    628 CCTCCAGCAGCAGAATGGGCTGTGCCTCAGTCATCAAGGCTGAAATACAGGCAGTTATTC
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               /sex="Male"
/cell_type="Embryonic stem cell"
/clone_lib="BayGenomics Gene Trap Library pGTlLxf"
/note="Vector: pGTlLxf"
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    2.6%; Score 94; DB 8; Length 94; 00.0%; Pred. No. 4.8e-12; ve 0; Mismatches 0; Indels
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    .94
    /organism="Mus musculus"

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                                                                                                                                 D18610
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BQ234483
AI947161
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                                                                                                         AI316382
CV295497
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                                                             AZ476761
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Location/Qualifiers
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/strain="129 ola"
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Best Local Si
Matches 94;
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9138_Full
1M0179F06
                                                                                 April 28, 2005, 06:48:09; Search time 10842.9 Seconds (without alignments) 12785.281 Million cell updates/sec
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CC200157 XG352 Bay
AZ786638 2M0032E18
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AZ614077 1
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CV030123
             GenCore version 5.1.6
Copyright (c) 1993 - 2005 Compugen Ltd.
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Maximum Match 100%
Listing first 45 summaries
                                                           nucleic search, using sw model
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Gapop 10.0 , Gapext 1.0
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9b est2: *
9b htc: *
9b est3: *
9b est4: *
9b est6: *
9b est6: *
9b gss1: *
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seq length: 100
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Score

Result 8 687

Gaps

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GSS 29-MAY-1997

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ACCESSION VERSION KEYWORDS SOURCE ORGANISM

REFERENCE AUTHORS TITLE JOURNAL COMMENT

LOCUS DEFINITION

RESULT 2 AA589590

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CC200157 46 bp mRNA linear GSS 09-MAY-2003
XG352 BayGenomics Gene Trap Library pGT1Lxf Mus musculus cDNA, mRNA
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 Direct Submission
Submitted (17-MAR-1995) Stylianos E. Antonarakis, Division of
Medical Genetics, University and Cantonal Hospital of Geneva, CMU,
1 rue Michel-Servet, 1211 Geneva, SWITZERLAND
Location/Qualifiers
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   Eukaryota, Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
Mammalia; Eutheria; Rodentia; Sciurognathi; Muridae; Murinae; Mus.
1 (bases 1 to 46)
                                                                                                                                                                                Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi; Mammalia; Eutheria; Primates; Catarrhini; Hominidae; Homo. I, Loases 1 to 64)
Chen, H., Chrast, R., Rossier, C., Morris, M.A., Lalioti, M.D. and Antonarakis, S.E.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            Contact: BayGenomics
Bay Area Functional Genomics Consortium (BayGenomics)
Email: info@baygenomics.ucsf.edu
Sequence tag generated by 5' RACE of total RNA from gene trap ES
cell line. ES cell lines harboring insertion mutation of target
gene are available upon request from BayGenomics. Annotation
                                                                                                                                                                                                                                                                                               Cloning of 559 potential exons of genes of human chromosome 21
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    1 GTCCCCAAGCAAGAACTATTCTTATGNAGTCAAGTTTACCACAGGCTCAGNTGGNTTCAA
  HSMC18D03 64 bp DNA linear GSS 29-M
H.sapiens DNA for trapped exon (ID HMC18D03), genomic survey
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/mol type="qenomic DNA"
                                                                                                                                                                                                                                                                                                                        exon trapping Genome Res. 6 (8), 747-760 (1996)
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            /mol_type="genomic DN/db_xref="taxon:9606"

    .64
/note="trapped exon"

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Unpublished (2001)
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Mus musculus
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Best Local Similarity 89.1%;
Matches 57; Conservative
                                                                                           X88324.1 GI:1437729
                                                                                                                                      Homo sapiens (human)
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                                                                                                                                   AA589590 16-SEP-1997 v149c09.sl Stratagene mouse skin (#937313) Mus musculus cDNA clone IMAGE:975568 3' similar to SW:YFJ4_YEAST P43603 HYPOTHETICAL 40.4 KD PROTEIN IN PES4-HIS2 INTERGENIC REGION. ;, mRNA sequence.
                                                                                                                                                                                                                                                                                                                                         Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Buteleostomi; Mammalia; Eutheria; Rodentia; Sciurognathi; Muridae; Murinae; Mus. 1 (bases 1 to 79)
Marra,M., Hillier,L., Allen,M., Bowles,M., Dietrich,N., Dubuque,T., Geisel,S., Kucaba,T., Lacy,M., Le,M., Martin,J., Morris,M., Schellenberg,K., Steptoe,M., Tan,F., Underwood,K., Moore,B., Theising,B., Wylie,T., Lennon,G., Soares,B., Wilson,R. and
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 9
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     Email: mouseest@watson.wustl.edu
This clone is available royalty-free through LLNL; contact the
This clone is available royalty-free through LLNL;
IMAGE Consortium (info@image.llnl.gov) for further information.
MGI:556296
Possible reversed clone: similarity on wrong strand
Seq primer: -28ml3 revl ET from Amersham
High quality sequence stop: 1.
Location/Qualifiers
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               Contact: Marra M/Mouse EST Project
WashU-HHMI Mouse EST Project
Washington University School of MedicineP
4444 Forest Park Parkway, Box 8501, St. Louis, MO 63108
Tel: 314 286 1800
Fax: 314 286 1810
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           2.0%; Score 74.2; DB 1; Length 79; 96.2%; Pred. No. 3.8e-07; ive 0; Mismatches 3; Indels
AACAGCCACGACAAAACTATGAGTGGACACTTAA 94
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/clone="IMAGE:975568"
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strain="C57BL/6"
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Matches 76; Conserv
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        AZ786638 16-FEB-2001
2M0032E18F Mouse 10kb plasmid UUGCIM library Mus musculus genomic
clone UUGC2M0032E18 F, genomic survey sequence.
information available from
http://baygenomics.ucsf.edu/cgi-bin/BaySearch.py?OPTION=EXACT&TYPE=
CELL_LINE&KEY=XG352
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  Mus musculus (house mouse)

Mus musculus

Bukaryota; Metazoa; Chordata; Craniata; Vertebrata; Buteleostomi;

Bukaryota; Metazoa; Chordata; Craniata; Vertebrata; Buteleostomi;

Mammalia; Butheria; Rodentia; Sciurognathi; Muridae; Murinae; Mus.

1 (bases 1 to 92)

1 (bases 2 to 92)

1 (bases 4 to 92)
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                Contact: Robert B. Weiss
University of Utah Genome Center
University of Utah
University of Utah
Rm. 308, Biomedical Polymers Research Bldg., 20 S. 2030 E., SLC,
84112, USA
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             /lab_host="E. Coli strain XL10-Gold, T1-resistant, F-"/clone lib="Mouse 10kb plasmid UTGCIM library."
/note="Wector: PWD4Zhry; Purified genomic DNA from M.musculus C57BL/6J (male) was obtained from the Jackson
                                                                                                                                                                                                                                                                                                                                                                                                        Gaps
                                                                                                                                                                                                                                           /cell_type="Embryonic stem cell"
/clone_lib="BayGenomics Gene Trap Library pGTILxf"
/note="Vector: pGT1Lxf"
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                                                                                                                                                                                                                                                                                                                                                                                                                                               300 TGTCATGAAACAGCAACCAGTGGCTATTTCCAGTGCACCAGCATTT 345
                                                                                                                                                                                                                                                                                                                                                                                                                                                                         1.3%; Score 46; DB 8; Length 46;
                                                                                                                                                                                                                                                                                                                                                                                                   0; Indels
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             Email: ddunn@genetics.utah.edu
Insert Length: 10000 Std Error: 0.00
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Seg primer: CGTTGTAAAACGACGGCCAGT
Class: plasmid ends
High quality sequence stop: 92.
Location/Qualifiers
                                                                                                                                   /organism="Mus musculus"
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          /organism="Mus musculus"
/mol_type="genomic DNA"
/strain="C57BL/63"
                                                                                                                                                        /mol_type="mRNA"
/strain="129 ola"
/db_xref="taxon:10090"
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                                                                  Class: Gene Trap.
Location/Qualifiers
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                                                                                                                                                                                                                             /sex="Male"
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                                                                                                                                                                                                                                                                                                                                                                               Best Local Similarity 100.0
Matches 46; Conservative
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   Tel: 801 585 5606
Fax: 801 585 7177
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      AZ786638
                                                                                                                                                                                                                                                                                                                                                            Query Match
                                                                                                                 Bource
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AZ786638/c
LOCUS
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KEYWORDS
SOURCE
ORGANISM
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                                                                                       FEATURES
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8 셤

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0.005 inch orifice at constant velocity. The sheared DNA was blunt end-repaired with T4 DNA polymerase and T4 polymuclectide kinase. Adaptor oligonuclectides were ligated to the blunt ends in high molar excess. The adaptored DNA was purified and size-selected for a 9.5 to 10.5 kb range using preparative agarose gel electrophoresis. Vector DNA was prepared from a derivative of pWD42 (gil4732114|gb|AF129072.1), a copy-number inducible derivative of plasmid R1. The vector was ligated with adaptors complementary to the insert adaptors and purified. The sheared, adaptored mouse DNA was annealed to adaptored vector DNA, and transformed into chemically-competent B. coli XL10-Gold (Stratagene) cells and selected for ampicillin resistance."
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University of Utah Genome Center
University of Utah
Genome Center
Winersity of Utah
Rm. 308, Biomedical Polymers Research Bldg., 20 S. 2030 B., SLC, UT
RM. 308, Blomedical Polymers Research
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   GSS 04-OCT-2000
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        A2448190
1M0245A17R Mouse 10kb plasmid UUGC1M library Mus musculus genomic clone UUGC1M0245A17 R, genomic survey sequence.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  /lab_host="B. Coli strain XL10-Gold, T1-resistant, F-"/clone_lib="Mouse 10kb plasmid UUGCIM library"/note="Vector: PWD42nv; Purified genomic DNA from M.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     0; Gaps
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      Query Match
1.2%; Score 44; DB 8; Length 92;
Best Local Similarity 67.4%; Pred. No. 13;
Matches 62; Conservative 0; Mismatches 30; Indels
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Seg primer: CACACAGGAAACAGCTATGACC
Class: plasmid ends
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/mol_type="genomic DNA"
/strain="C57BL/6J"
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                /db_xref="taxon:10090"
/clone="UUGC1M0245A17"
/sex="Male"
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    Email: ddunn@genetics.utah.edu
Insert Length: 10000 Std Erro
Plate: 0245 row: A column: 17
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Location/Qualifiers
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Mus musculus
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AZ448190.1 GI:10600743
GSS.
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Unpublished (2000)
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Fax: 801 585 7177
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AZ804535
AZ804535.1 GI:12956858
                                                                                                                                                                                                                                19 GAAGCAGGAGGAGAAG 1
L Similarity 69.6%;
55; Conservative
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  Class: plasmid ends
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  plasmid inserts
Unpublished (2000)
Best Local Similarity
Matches 55; Conserv
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DEFINITION
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VERSION
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COMMENT
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AZ804535
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                                          (http://www.jax.org/resources/documents/dnares/). The DNA was hydrodynamically sheared by repeated passage through a 0.005 inch orifice at constant velocity. The sheared DNA was blunt end-repaired with T4 DNA polymerase and T4 polymucleotide kinase. Adaptor oligonucleotides were ligated to the blunt ends in high molar excess. The adaptored DNA was purified and size-selected for a 9.5 to 10.5 kb range using preparative agarose gel electrophoresis. Vector DNA was prepared from a derivative of pMAP12 (gil 4732114|gb|AR12972.1); a copy number inducible derivative of plasmid R1. The vector was ligated with adaptors complementary to the insert adaptors and purified. The sheared, adaptored mouse DNA was annealed to adaptored vector DNA, and transformed into chemically-competent E. coli Xiii0-Gold (Stratagene) cells and selected for ampicillin resistance."
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Asamizu, E., Nakamura, Y., Sato, S. and Tabata, S.
A large scale analysis of cDNA in Arabidopsis thaliana: Generation
of 12,028 non-readment expressed sequence tags from normalized and
size-selected cDNA libraries
DNA Res. 7 (3), 175-180 (2000)
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               The First Laboratory for Plant Gene Research
Kazusa DNA Research Institute
Yana 1532-3, Kiaszazu, Chiba 292-0812, Japan
Email: asamizu@kazusa.or.jp, URL:http://www.kazusa.or.jp/en/plant/.
Location/Qualifiers
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           AV533640 Arabidopsis thaliana flower buds Columbia Arabidopsis thaliana cDNA clone FB065d08F 3', mRNA sequence.
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            Arabidopsis thaliana
Mukaryota, Viridiplantae, Streptophyta, Embryophyta, Tracheophyta,
Spermatophyta, Magnoliophyta, eudicotyledons, core eudicots,
rosids, eurosids II, Brassicales, Brassicaceae, Arabidopsis.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  /tissue type="flower buds"
/clone lib="Arabidopsis thaliana flower buds Columbia"
/note="Vector: pBluescriptII SK-; Site_1: BcoRI; Site_2:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             musculus C57BL/6J (male) was obtained from the Jackson
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   Gaps
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1.2%; Score 42.8; DB 8; Length 89;
Best Local Similarity 68.6%; Pred. No. 25;
Matches 59; Conservative 0; Mismatches 27; Indels
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              organism="Arabidopsis thaliana"
                               Laboratory Mouse DNA Resource
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/clone="FB065d08F"
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/ecotype="Columbia"
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       Contact: Erika Asamizu
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AUTHORS
TITLE
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PUBMED
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KEYWORDS
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DRIGIN

임 ð 1.1%; Score 40.6; DB 1; Length 86;

Query Match

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(http://www.jax.org/resources/documents/dnares/). The DNA was hydrodynamically sheared by repeated passage through a 0.005 inch oritice at constant velocity. The sheared DNA was blunt end-repaired with T4 DNA polymerase and T4 polymucleotide kinase. Adaptor oligonucleotides were ligated to the blunt ends in high molar excess. The adaptored DNA was purified and size-selected for a 9.5 to 10.5 kb range using preparative agarose gel electrophoresis. Vector DNA was prepared from a derivative of pWD42 (gi |4732114|gb|AP129072.1), a copy-number inducible derivative of plasmid R1. The vector was ligated with adaptors complementary to the insert adaptors and purified. The sheared adaptored mouse DNA was annealed to adaptored vector DNA, and transformed into adaptored vector DNA, and transformed into chemically-competent B. coli XL10-Gold (Stratagene) cells
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                                                                                              1200 GGAGGCCAAGCGGCAGCTGGAGCTGGAGAGCTGGAGAAGCAGCGGGAGCTGGAGCG
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Junn, D., Aoyaqi, A., Barber, M., Beacorn, T., Duval, B., Hamil, C., Islam, H., Longacre, S., Mahmoud, M., Meenen, E., Pedersen, T., Nickelly, M., Rose, M., Rose, M., Rose, R., Stokes, R., Tingey, A., von Niederhausern, A. and Wright, D., Weiss, R.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        AZ804535
2M0065121R Mouse 10kb plasmid UUGC1M library Mus musculus genomic clone UUGC2M0065121 R, genomic survey sequence.
                                                                                                                                                                          79 GGAGGAGAAGCAACGGGAGGAGGAGGAAGCGACTGGAGGAGGAGGAGTAGCTGGAGGA 20
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 from the Jackson
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                                  0; Gaps
                                  24; Indels
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Fax: 801 585 7177
Email: ddunmgenetics.utah.edu
Insert Length: 10000 Std Error: 0.00
Plate: 0065 row: I column: 21
Pred. No. 87;
0; Mismatches
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Seq primer: CACACAGGAAACAGCTATGACC
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/mol_type="genomic DNA"
/strain="C57BL/6J"
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University of Utah Genome Center
University of Utah
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/clone="UUGC2M0065121"
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Location/Qualifiers
                                                                                                                                                                                                                                                     1260 GCAGCGAGAGGAGAGG 1278
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Best Local Similarity
Matches 49; Conserv
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                                                                                                                                                                                 Query Match
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AZ837486/c
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KEYWORDS
SOURCE
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                                                                                                                                                                                                                                                                                                                                                                                                                                                             AZ471347 100 DNA linear GSS 04-OCT-2000 1M0285121R Mouse 10kb plasmid UUGCIM library Mus musculus genomic clone UUGCIM0285121 R, genomic survey sequence.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      Contact: Robert B. Weiss
University of Utah Genome Center
University of Utah
Wm. 308, Biomedical Polymers Research Bldg., 20 S. 2030 E., SLC, UT
84112, USA
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                                                                                                                                                                           1199 AGGAGGCCAAGCGGCAGCTGGAGCTGGAGAAGCTGGAGAAGCAGCGGGAGCTGGAGC 1258
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Dunn, D., Aoyagi, A., Barber, M., Beacorn, T., Duval, B., Hamil, C., Islam, H., Longacre, S., Mahmoud, M., Meenen, E., Pedersen, T., Nese, M., Rose, R., Stokes, R., Tingey, A., von Niederhausern, A. and Wright, D., Weise, R.
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/note="Vector: PWD42nv; Purified genomic DNA from M.
musculus C57BL/6J (male) was obtained from the Jackson
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         /lab_host="E. Coli strain XL10-Gold, T1-resistant, F-"
                                                                                                                                                                                                                              Gaps
                                                                                                                              ;
0
                                                                           Length 94;
                                                                        Query Match 1.1%; Score 40.4; DB 8; Length 9
Best Local Similarity 65.6%; Pred. No. 1e+02;
Matches 59; Conservative 0; Mismatches 31; Indels
and selected for ampicillin resistance."
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    Email: ddunn@genetics.utah.edu
Insert Length: 10000 Std Brror: 0.00
Plate: 70285 row: I column: 21
Seg primer: CACACAGGAAACAGCTATGACC
Class: plasmid ends
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                                                                                                                                                                                                                                                                                    1259 GGCAGCGAGGAGGAGGAGGAGGAGA 1288
                                                                                                                                                                                                                                                                                                                                  62 AGGAGGAGGAGGAGGAGGAGGAGA 91
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/strain="CS7BL/6J"
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        High quality sequence stop: 71.
Location/Qualifiers
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            Mus musculus (house mouse)
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         AZ471347.1 GI:10629472
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             Unpublished (2000)
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Fax: 801 585 7177
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AZ471347/c
LOCUS
DEFINITION
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KEYWORDS
SOURCE
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TITLE

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(http://www.jax.org/resources/documents/dnares/). The DNA was hydrodynamically sheared by repeated passage through a 0.005 inch orifice at constant velocity. The sheared DNA was blunt end-repaired with T4 DNA polymerase and T4 polynucleotide kinase. Adaptor oligonucleotides were ligated to the blunt ends in high molar excess. The adaptored DNA was purified and size-selected for a 9.5 to
with adaptors complementary to the insert adaptors and purified. The sheared, adaptored mouse DNA was annealed to adaptored vector DNA, and transformed into chemically-competent B. coli Xi10-Gold (Stratagene) cells and selected for ampicillin resistance."
                                                                                                                                                                                                                                                                                                                                                                             1219 GAGCTGGAGAAGCAGCTGGAGAAGCAGCGGGAGCTGGAGCGGCAGCGAGGAGGAGGAGAGG 1278
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          Rm. 308, Biomedical Polymers Research Bldg., 20 S. 2030 E., SLC, UT
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2M0132J14R Mouse 10kb plasmid UUGCIM library Mus musculus genomic clone UUGC2M0132J14 R, genomic survey sequence.
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/clone_lbb="Mouse lokb plasmid UUGCIM library"
/note="Vector: PWD42nv; Purified genomic DNA from M.
musculus C57BL/6J (male) was obtained from the Jackson
                                                                                                                                                                                                                                                                                                                                                                                                                          1.0%; Score 36.4; DB 8; Length 71; ilarity 70.0%; Pred. No. 9.1e+02; Conservative 0; Mismatches 21; Indels
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Insert Length: 10000 Std Brror: 0.00
Plate: 0132 row: J column: 14
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Seg primer: CACACAGGAAACAGCTATGACC
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/mol_type="genomic DNA"
/strain="C57BL/6J"
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       Contact: Robert B. Weiss
University of Utah Genome Center
University of Utah
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Location/Qualifiers
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Mus musculus
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Unpublished (2000)
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Fax: 801 585 7177
Email: ddunn@qenet
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electrophoresis. Vector DNA was prepared from a derivative of pWD42 (gi|4732114] pA PAT290721.), a copy-number of pMD42 (gi|4732114] pD | APT290721.), a copy-number inducible derivative of plasmid R1. The vector was ligated with adaptors complementary to the insert adaptors and ppurified. The sheared, adaptored mouse DNA was annealed to adaptored vector DNA, and transformed into chemically-competent B. coli X11.0-Gold (Stratagene) cells and selected for ampicillin resistance."
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Mammalia; Eutheria; Rodentia; Sciurognathi; Muridae; Murinae; Mus.
1 (bases 1 to 91)
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/clone lib="Mouse 10kb plasmid UTGCIM library"
/note="Vector: PWD42Iv; Purified genomic DNA from M.
musculus C57BL/6J (Male) was obtained from the Jackson
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                                                                                                                                                                                                                                                                                                                                                                                                                                              Dunn, D., Aoyagi, A., Barber, M., Beacorn, T., Duval, B., Hamil, C., Islam, H., Longacre, S., Mahmoud, M., Meenen, E., Pedersen, T., Reilly, M., Rose, M., Rose, R., Stokes, R., Tingey, A., von Niederhausern, A. and Wright, D., Weiss, R. Mouse whole genome scaffolding with paired end reads from 10kb plasmid inserts
                                                                                                                                                                                                                                                                                                                                                          Gaps
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0
                                                                                                                                                                                                                                                                                                  1.0%; Score 36.2; DB 8; Length 87; 68.5%; Pred. No. 1.1e+03; tive 0; Mismatches 23; Indels
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Class: plasmid ends
High quality sequence stop: 91.
Location/Qualifiers
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/organism="Mus musculus"
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University of Utah Genome Center
University of Utah
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Length: 10000 Std Brro
0442 row: B column: 14
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Fax: 801 585 7177
Email: ddunn@genet
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Best Local Similarity
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was blunt end-repaired with T4 DNA polymerase and T4 polynucleotide kinase. Adaptor oligonucleotides were ligated to the blunt ends in high molar excess. The adaptored DNA was purified mad size-selected for a 9.5 to 10.5 kb range using preparative agarose gel electrophoresis. Vector DNA was prepared from a derivative of pWD42 (gi|4732114|gb|AF129072.1), a copy-number inducible derivative of plasmid R1. The vector was ligated with adaptors complementary to the insert adaptors and purified. The sheared, adaptored mouse DNA was annealed to adaptored vector DNA, and transformed into chemically-competent E. coli XL10-GGld (Stratagene) cells and selected for ampicillin resistance."
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/wollivar="mixed background W23/A188/B73"
/db_xref="taxon:4577"
/tissue_type="leaf"
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/dar_bost="mixed background Grid G"
/lab_host="mixed"
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/lab_host="mixed"
/lab_host="lorgan: leaf; Vector: RescueMu (engineered from pBusescript backbone); Site_1: BamHI; Site_2: BglII; RescueMu is a 4.9 kb, modified maize Mu transposon designed to allow plasmid rescue from total genomic DNA. Mu elements insert preferentially into transcription units. For more information on RescueMu, go to the web site 'www.zmdb.iastate.edu' and follow the links for
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Contact: Walbot V
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(bases 1 to 91)
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Possible ligation site so sequence was trimmed. Post-ligation
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Fax: 650 725 8221
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Stanford University
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/organism="Zea mays"
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Unpublished (2001)
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Spermatophyta, Magnoliophyta, Liliopsida, Poales, Poaceae, PACCAD
clade, Panicoideae, Andropogoneae, Zea.
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Fax: 650 725 8221
Email: walbot@stanford.edu
Possible ligation site so sequence was trimmed. Post-ligation
sequence submitted separately.
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/cultivar="mixed background W23/A188/B73"
/db_xref="taxon:4577"
/fisue_type="leaf"
/dev stage="adult"
/lab_host="DH10B"
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                                64.3%; Pred. No. 1.2e+03;
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1006126H07,x1.1006 - RescueMu Grid
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'RescueMu.' Grid G was grown at Stanford in 2000. DNA was extracted from leaf punches, double digested using BamHI and Bill, and ligated to form circular plasmids. DH10B cells were transformed and then screened on LB plates with ampicillin."
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Spermatophyta, Magnoliophyta, Liliopsida, Poales, Poaceae, PACCAD
clade, Panicoideae, Andropogoneae, Zea.
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/lab_host="DH10B"
/clone_lib="1006 - RescueMu Grid G"
/clone_lib="1006 - RescueMu Grid G"
/note="Organ: leaf; Vector: RescueMu (engineered from pBlueScript backbone); Site 1: BamHI; Site 2: BgIII;
RescueMu is a 4.9 kb, modified maize Mu transposon designed to allow plasmid rescue from total genomic DNA.
Mu elements insert preferentially into transcription units. For more information on RescueMu, go to the web site 'www.zmdb.iastate.edu' and follow the links for
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Class: transposon-tagged.
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/cultivar="mixed background W23/A188/B73"
/db xref="taxon:4577"
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Tel: 650 723 2227
Fax: 650 725 8221
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64.3%; Pred. No. 1.2e+03;
tive 0; Mismatches 30;
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Contact: Walbot V
Department of Biological Sciences
Stanford University
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                                                                                                                                                                                                                                                                               Local Similarity
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                                                                                                                                                                                                                                                  Query Match
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BH225515/c
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Matches
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TITLE
JOURNAL
COMMENT
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                ACCESSION
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KEYWORDS
SOURCE
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1175

56

1176 GAAAGAGGGGGGGGCGCCAGGAGCA 1199

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DB 8; Length 91;

1.0%; Score 36;

Query Match

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Gaps

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CR272899 96 bp DNA linear GSS 06-JUL-2004 Forward strand read from insert in 5'HPRT insertion targeting and chromosome engineering clone MHPN79102, genomic survey sequence.
                                                                                                                                                                                                                                                                                                                    Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Buteleostomi; Mammalia; Eutheria; Rodentia; Sciurognathi; Muridae; Murinae; Mus. 1 (bases 1 to 96) adams, D.J., Biggs, P.J., Cox, A.V., Davies, R.M., van der Weyden, L., Roders, J., Smith, J., Plumb, R.W., Taylor, R.G., Nishijima, I., Yu, Y., Rogers, J., and Bradley, A. Davies, Taylor, R.G., Nishijima, I., Yu, Y., Buter Submitted (20-FBB-22004) Sanger Centre, Hinxton, Cambridgeshire, CB10 18A, UK. http://www.sanger.ac.uk/MICER
                                                                                                                                                                                                                                                      GSS; genome survey sequence; MICER.
Mus musculus (house mouse)
Mus musculus
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            1. 96 // Organism="Mus musculus" /organism="Mus musculus" // mol_type="genomic DNA" /db Xref="taxon:10090" /clone="MHPN79102" /clone_lib="MHPN"
25 GAAGACCCAGGAGCCGCCGCAGCA 2
                                                                                                                                                                                                                                     CR272899.1 GI:50051754
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VERSION
KEYWORDS
SOURCE
ORGANISM
                                                                                              RESULT 15
CR272899/c
LOCUS
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 source
                                                                                                                                                               DEFINITION
                                                                                                                                                                                                                                                                                                                                                                          REFERENCE
AUTHORS
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JOURNAL
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         FEATURES
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1267 GAGGAGGAGGAAGGAAGGAGATCGAGAGG 1296 35 AĞAĞĞĞAĞĞĞAĞĞAĞĞAĞĞAĞĞAĞĞĞĞ 셤 ð 셤

1207 AAGCGGCAGCTGGAGCTGGAGAAGCAGCTGGAGAAGCAGCGGGAGCTGGAGCGGCAGCGA 1266

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Query Match
1.0%; Score 35.6; DB 9; Length 96;
Best Local Similarity 62.2%; Pred. No. 1.6e+03;
Matches 56; Conservative 0; Mismatches 34; Indels

Gaps . 0

Search completed: April 29, 2005, 02:01:58 Job time : 10843.9 secs

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GenCore version 5.1.6
Copyright (c) 1993 - 2005 Compugen Ltd.
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OM nucleic - nucleic search, using sw model

Run on:

April 28, 2005, 07:02:07; Search time 544.672 Seconds (without alignments) 10941.112 Million cell updates/sec

US-09-674-237B-2 3642

Perfect score:

1 atggctcagtttcccacacc......tggaccccagccagcaatga 3642 Sequence:

IDENTITY NUC Gapop 10.0 , Gapext 1.0 Scoring table:

1202784 seqs, 818138359 residues Searched:

1330268 Total number of hits satisfying chosen parameters:

seq length: 0 seq length: 100 Minimum DB Maximum DB

Post-processing: Minimum Match 0% Maximum Match 100% Listing first 45 summaries

Database :

Issued Patents NA:\*

(cgn2\_6/ptodata/1/ina/5A\_COMB.seq:\*
(cgn2\_6/ptodata/1/ina/5B\_COMB.seq:\*
(cgn2\_6/ptodata/1/ina/6A\_COMB.seq:\*
(cgn2\_6/ptodata/1/ina/6B\_COMB.seq:\*
(cgn2\_6/ptodata/1/ina/PcTUS\_COMB.seq:\*
(cgn2\_6/ptodata/1/ina/PcTUS\_COMB.seq:\*

Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

## SUMMARIES

			, de			SUMMAKIES	
Result No.	t	Score	Query	Query Match Length DB	DB	OI	Description
	-	38	1.0	78	m	US-09-043-303-12	Sequence 12, Appl
	0	37.6	1.0	69	4	US-09-573-080A-463	463,
	۳	36.4	1.0	78	m	US-09-043-303-11	11,
	4	34	0.9	75	ო	US-09-043-303-10	10,
	ß	33	6.0	69	ო	US-09-043-303-13	13,
	9	32.2	6.0	69	4	US-09-573-080A-462	462,
υ	7	31.4	6.0	89	4	US-09-270-767-4823	482
U	œ	31.4	6.0		4	US-09-270-767-20105	
	σ	30.4	0.8	93	æ	US-08-556-978B-24	
υ	10	30.4	0.8	93	m	US-08-556-978B-25	.,
υ	11	30.2	0.8	51	ч	US-08-068-747-1	•
	12	30	0.8	98	4	US-09-513-999C-14585	Sequence 14585, A
	13	29.4	0.8	57	7	US-07-814-220-26	.,
	14	29.4	0.8	57	N	US-07-812-421-26	Sequence 26, Appl
Ö	15	29.4	0.8	62	N	US-07-814-220-25	25,
υ	16	29.4	0.8	62	~	US-07-812-421-25	Sequence 25, Appl
1	17	29.4	0.8	97	П	US-08-182-175A-48	48,
-	18	29.4	0.8	97	7	US-08-474-633A-57	57,
-	19	29.4	0.8	97	m	US-08-823-771-57	S
. •	20	29.4	0.8	97	Ŋ	PCT-US92-06412-48	48,
υ	21	σ	0.8	99	4	US-09-402-532-21	77
υ		29	0.8	96	ო	US-09-281-481A-6	w
		29		96	m	9-281-	7,
. •	24	28.6	0.8	78	4	-09-513-999C-355	(*)
	22	28.4	•	94	4	US-09-513-999C-29269	Sequence 29269, A
	56		0.8	57	m	US-09-043-303-14	14,
• •	2.2	28.2	0.8	28	m	US-08-860-038-15	Sequence 15, Appl

Appl	Appl	Appl	Appl	Appl	Appl	Appl	Appl	Appl	Appl	Appl	Appl	Appl	Appl	Appl	Appl	Appl	Appli
15,	88	65,	65,	88	25,	23,	58,	29,	58,	25,	25,	58,	89,	99	99	89	5
Sequence	Sequence	Sequence	Sequence	Sequence	Sequence	Sequence	Sequence	Sequence	Sequence	Sequence	Seguence	Sequence	Sequence	Sequence	Sequence	Sequence	Sequence
US-09-580-923-15	US-08-182-175A-88	US-08-474-633A-65	US-08-823-771-65	PCT-US92-06412-88	US-07-609-716-25	US-08-175-155-23	US-08-477-509B-58	US-08-707-237A-29	US-08-482-085B-58	US-08-475-411A-25	US-08-478-029A-25	US-09-444-791A-58	US-08-182-175A-89	US-08-474-633A-66	US-08-823-771-66	PCT-US92-06412-89	US-07-941-651-5
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28	84	84	84	84	68	89	68	68	68	68	69	68	84	84	84	84	75
9.0	8.0	8.0	8.0	9.0	8.0	8.0	9.0	9.0	8.0	8.0	9.0	8.0	8.0	8.0	0.8	9.0	9.0
28.2	28.2	28.2	28.2	28.5	28	28	28	28	28	28	28	28	28	28	28	28	27.8
28	53	30	31	32	33	34	35	36	37	38	33	40	41	42	43	44	45
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## ALIGNMENTS

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Sequence 12, Application US/09043303

Patent No. 6251589

GENERAL INFORMATION:
APPLICANT: SANPEI, Kazujiro
TITLE OF INVENTION: Method for Diagnosing Spinocerebellar Alaxia Type 2 and
TITLE OF INVENTION: Primers Therefor
TITLE OF INVENTION: Primers Therefor
FILE REFERENCE: 0760-0241P
CURRENT APPLICATION NUMBER: US/09/043,303
CURRENT PILING DATE: 1998-05-18
EARLIER APPLICATION NUMBER: PCT/JP96/01999
MUMBER OF SEQ ID NOS: 17
SOFTWARE: Patentin Ver. 2.0
SEQ ID NO 12
LENGTH: 78
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                                                                                                                                                                                                                                                                                                                                                                                                   TYPE: DNA
ORGANISM: Homo sapiens
RESULT 1
US-09-043-303-12
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1252 CTGGAGCGCCAGCGAGAG 1269 ò

cadcadecedeceded 78 61 셤 RESULT 2
US-09-573-080A-463

i Sequence 463, Application US/09573080A

j Patent No. 6828097

GENERAL INFORMATION:
APPLICANT: JOAN, KNOLL

TITLE OF INVENTION:
FILE REPRENCE: 30307

CURRENT APPLICATION UNBER: US/09/573,080A

CURRENT PILICATION DATE: 2000-05-16

NUMBER OF SEQ ID NOS: 479

SEQ ID NO 463

LENGTH: 69

Gaps ;

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1196 AGCAGGAGGCCAAGCGGCAGCTGGAGCTGGAACCAGCTGGAAAGCAGCGGGAGCTGG 1255
                                                                                                                                                                                                                                  Query Match 0.9%; Score 34; DB 3; Length 75; Best Local Similarity 66.2%; Pred. No. 41; Matches 49; Conservative 0; Mismatches 25; Indels
                                                                                                                                                                                                                                                                              1256 AGCGGCAGCGAGAG 1269
LENGTH: 75
TYPE: DNA
ORGANISM: Homo sapiens
                                                                  US-09-043-303-10
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LENGTH: 69
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                                              PEATURE:
OTHER INFORMATION: Description of Artificial Sequence: repetitive sequence found in
OTHER INFORMATION: many eutherial genomes. Length of core repeating element is vari
OTHER INFORMATION: able and is often polymorphi
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    Sequence 11, Application US/09043303
Sequence 11, Application US/09043303
Sequence 11, Application US/09043303
Sequence 11, Application US/09043303
TEREAL INFORMATION: Method for Diagnosing Spinocerebellar Alaxia Type 2 and TITLE OF INVENTION: PHILE STREENCE: 0760-0241P
TITLE OF INVENTION: PHILES THEREOUS: 0760-0241P
CURRENT APPLICATION NUMBER: US/09/043,303
CURRENT FILING DATE: 1998-05-18
EARLIER FILING DATE: 1996-07-18
NUMBER OF SEQ ID NOS: 17
SOFTWARE: Patentin Ver. 2.0
SEQ ID NO 11
LENGTH: 78
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   Sequence 10, Application US/09043303
; Sequence 10, Application US/09043303
; Patent No. 6251589
; GENERAL INFORMATION:
; APPLICANT: TSUJI, Shoji
; APPLICANT: SANPEI, Kazujiro
TITLE OF INVENTION: Method for Diagnosing Spinocerebellar Alaxia Type 2 and
TITLE OF INVENTION: Primers Therefor
; TITLE OF INVENTION: Primers Therefor
; FILE REFERRINCE: 0760-0241P
; CURRENT APPLICATION NUMBER: US/09/043,303
; CURRENT FILING DATE: 1996-05-18
; EARLIER FILING DATE: 1996-07-18
; NUMBER OF SEQ ID NOS: 17
; SOFTWARE: Patentin Ver. 2.0
; SEQ ID NO 10
                                                                                                                                                                                                                                                             1197 GCAGGAGGCCAAGCGGCAGCTGGAGCAGCAGCTGGAGAAGCAGCGGGAGCTGGA 1256
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Pred. No. 4.4;
                                                                                                                                                                                                                  0; Mismatches
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Best Local Similarity 72.15
Matches 49; Conservative
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ORGANISM: Homo sapiens
                                                                                                                                                                                                                                                                                                                                                                                         GCAGCAGC 68
    TYPE: DNA ORGANISM: Artificial
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              Best Local Similarity
Matches 52; Conserv
                                                                                                                     ; OTHER INFORMAT
US-09-573-080A-463
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US-09-043-303-10
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US-09-043-303-11
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SINGLE COPY GENOMIC HYBRIDIZATION PROBES AND METHOD OF GENERATIA
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                                                                                                                                                                                                               APPLICANT: TSUJI, Shoji
APPLICANT: TSUJI, Shoji
APPLICANT: SANPEI, Kazujiro
TITLE OF INVENTION: Method for Diagnosing Spinocerebellar Alaxia Type 2 and
TITLE OF INVENTION: Primers Therefor
FILE REFERENCE: 0760-0241P
CURRENT APPLICATION NUMBER: US/09/043,303
CURRENT FILING DATE: 1998-05-18
EARLIER APPLICATION NUMBER: PCT/JP96/01999
EARLIER FILING DATE: 1996-07-18
NUMBER OF SEQ ID NOS: 17
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 1208 AGCGGCAGCTGGAGCTGGAGAAGCAGCTGGAGAAGCAGCGGGAGCTGGAGCGGCAGC 1264
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     CURRENT APPLICATION NUMBER: US/09/573,080A CURRENT FILING DATE: 2000-05-16 NUMBER OF SEQ ID NOS: 479 SOFTWARE: PatentIn version 3.0
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   US-09-573-080A-462; Application US/09573080A; Sequence 462, Application US/09573080A; Datent No. 6828097; GENERAL INFORMATION: APPLICANT: DOAN, ENOLL; TITLE OF INVENTION: SINGLE COFY GENOMI; FILE REFERENCE: 30307
                                                                                                          US-09-043-303-13
; Sequence 13, Application US/09043303
; Patent No. 6251589
; GENERAL INFORMATION:
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Best Local Similarity 73.7%;
Matches 42; Conservative (
62 Adccdccdcccccc 75
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              SOFTWARE: Patentin Ver. 2.0
SEQ ID NO 13
LENGTH: 69
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        TYPE: DNA ORGANISM: Homo sapiens
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         ORGANISM: Artificial
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FILING DATE:
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                                                                                                                                                                                                                                                                                                                COUNTRY:
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                                                             1209 GCGCCAGCTGGAGCTGGAGAAGCAGCTGGAGAAGCAGCGGGAGCTGGAGCGGCAGCGAGA 1268
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                                                                                                    81 GCGCCCCTGGAGCTGGAGCAGGAGCCGAGATCACCACGGGTGCTGGAGGAGCAAGGGAC 22
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                                                                                                                                                                                                                                                                                  Sequence 4823, Application US/09270767
Patent No. 6703491
GENERAL INFORMATION:
GENERAL INFORMATION:
TITLE OF INVENTION: Nucleic acids and proteins of Drosophila melanogaster FILE REFERENCE: File Reference: 7326-094
CURRENT FILING DATE: 1999-03-17
NUMBER OF SEQ ID NOS: 62517
SOFTWARE: PatentIn Ver. 2.0
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           Sequence 20105, Application US/09270767

Patent No. 6703491

GENERAL INFORMATION

APPLICANT: Homburger et al.

TITLE OF INVENTION: Nucleic acids and proteins of Drosophila melanogaster FILE REPRENCE: File Reference: 7326-094

CURRENT APPLICATION NUMBER: US/09/270,767

CURRENT FILING DATE: 1999-03-17

NUMBER OF SEQ ID NOS: 62517

SOFTWARE: PatentIn Ver. 2.0

SEQ ID NO 20105

LENGTH: 89
                             Gaps
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61.7%; Pred. No. 2.2e+02;
tive 0; Mismatches 31; indels
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Pred. No. 2.2e+02;
0; Mismatches 31; Indels
                         23; Indels
Best Local Similarity 66.7%; Pred. No. 1.2e+02; Matches 46; Conservative 0; Mismatches 23
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ORGANISM: Drosophila melanogaster
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   , ORGANISM: Drosophila melanogaster US-09-270-767-20105
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1 Similarity 61.7%;
50; Conservative
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Matches 50; Conservative
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Best Local Similarity
Matches 50; Conserva
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US-09-270-767-20105/c
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LENGTH: 89
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1708 GCCTTGGAAGCAAAGGAGCTGGCCCGGCAGCACCTCCGGGAGCAGCTGGACGAGGT 1763
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Sequence 24, Application US/08556978B

Sequence 24, Application US/08556978B

Ratent No. 6268169

Fater No. 6268169

TITLE OF INVENTION: SPIDER SILK ANALOGS

INVERSE OF SEQUENCES: 107

CORRESPONDENCE ADDRESS:

ADDRESSEE: E. I. DU PONT DE NEMOURS AND COMPANY

STREET: 1007 MARKET STREET

CITY: WILMINTON

STATE: DELAWARE
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     : E. I. DU PONT DE NEMOURS AND COMPANY
1007 MARKET STREET
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        GENERAL INFORMATION:
APPLICANT: FAHNESTOCK, STEPHEN F.
TITLE OF INVENTION: NOVEL RECOMBINANTLY PRODUCED
TITLE OF INVENTION: SPIDER SILK ANALOGS
NUMBER OF SEQUENCES: 107
CORRESPONDENCE ADDRESS:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      16;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   Score 30.4; DB 3;
Pred. No. 4.1e+02;
0; Mismatches 16;
                                                                                                                                                                                                                                                                                                                                                                                MEDIUM TYPE: DISKETTE, 3.50 INCH
COMPUTER: IBM PC COMPATIBLE
OPBRATING SYSTEM: MICROSOFT WINDOWS 95
SOFTWARE: MICROSOFT WORD FOR WINDOWS 95
CURRENT APPLICATION DATA:
APPLICATION NUMBER: US/08/556,978B
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         CLASSIFICATION: 435
PRIOR APPLICATION DATA:
RAPLICATION NUMBER: 08/077,600
FILING DATE: JUNE 15, 1993
ATTORNEY/AGENT INFORMATION:
NAME: FLOYD. LINDA AXAMETHY
REGISTRATION NUMBER: 33,692
REFERENCE/DOCKET NUMBER: CR-9389-A
TELECHONE: 302-892-8112
TELEPHONE: 302-773-0164
                                                                                                                                                                                                                                                                                                              UNITED STATES OF AMERICA
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        STREET: 1007 MARKET STREET
COUTY: WILMINTON
STATE: DELAMARE
COUNTRY: UNITED STATES OF AMERICA
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          COMPUTER READABLE FORM:
MEDIUM TYPE: DISKETTE, 3.50 INCH
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 RESULT 10
10S-08-556-978B-25/c
; Sequence 25, Application US/08556978B
; Patent No. 6268169
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               MOLECULE TYPE: DNA (genomic)
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   Query Match 0.8%;
Best Local Similarity 71.4%;
Matches 40; Conservative
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                TYPE: nucleic acid
STRANDEDNESS: single
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0; Gaps

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1207 AAGCGGCAGCTGGAGCTGGAGAAGCAGCTGGAAAACAGCGGGAGCTGGAGCGGCAGCGA 1266
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Squence 14585, Application US/09513999C

GENERAL INFORMATION:
APPLICANT: Duclert, A.
APPLICANT: Duclert, A.
APPLICANT: Giordano, J.Y.
FILLE REFERENCE: 59.US2.REG
CURRENT APPLICATION NUMBER: US/09/513,999C
CURRENT FILING DATE: 2000-02-24
PRIOR APPLICATION NUMBER: US 60/122,487
PRIOR APPLICATION NUMBER: US 60/122,487
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  4 AAGCGGCGTCGGCGCTCGGAGCAGCAGCAGCCGNACGAGCAGCGGAGGCGRTCGGGA
                                                                                                                                                                                           1213 CAGCTGGAGCTGGAGCAGCTGGAGAAGCAGCGGGAGCTGGAGCGGCAG 1263
                                                                                                                                                                                                                                      Sequence 26, Application US/07814220

Patent No. 592540

GENERAL INFORMATION:
APPLICANT: Caccci, Thomas E.
APPLICANT: Toth, Thomas E.
APPLICANT: Szumanski, Maria B.W.
TITLE OF INVENTION: SYNTHETIC GENE CODING FOR ITS PRODUCTION NUMBER OF SEQUENCES: 43
CORRESPONDENCE ADDRESS:
                                                                                                    Query Match 0.8%; Score 30.2; DB 1; Length 51; Best Local Similarity 74.5%; Pred. No. 3.2e+02; Matches 38; Conservative 0; Mismatches 13; Indels
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 ADDRESSEE: WHITHAM, CURTIS & WHITHAM STREET: Reston Intl. Center, 11800 Sunrise Valley Dr., STREET: Suite 900
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    DB 4; Length 86;
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----- 32; Indels
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1; Mismatches
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                  MOLECULE TYPE: other nucleic acid DESCRIPTION: /desc = "synthetic"
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Best Local Similarity 59.3%;
Matches 48; Conservative
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US-09-513-999C-14585
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   NUMBER OF SEQ ID NOS: 36681
SOFTWARE: Patent.pm
SEQ ID NO 14585
LENGTH: 86
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LOCATION: 40
OTHER INFORMATION: n=a, 9
FEATURE: misc_feature
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US-09-513-999C-14585
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                                                               US-08-068-747-1
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APPLICANT: Schalling, Martin
APPLICANT: Hudson, Thomas J.
APPLICANT: Hudson, Thomas J.
APPLICANT: Housen, David E.
TITLE OF INVENTION: Direct Determination of Expanded
TITLE OF INVENTION: Nucleotide Repeats in the Human Genome
NUMBER OF SEQUENCES: 11
CORRESPONDENCE ADDRESS:
ADDRESSE: Hamilton, Brook, Smith & Reynolds, P.C.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   Length 93;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 16; Indels
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   Query Match 0.8%; Score 30.4; DB 3; Best Local Similarity 71.4%; Pred. No. 4.1e+02; Matches 40; Conservative 0; Mismatches 16;
OPERATING SYSTEM: MICROSOFT WINDOWS 95
SOFTWARE: MICROSOFT WORD FOR WINDOWS 95
CURRENT APPLICATION DATA:
APPLICATION NUMBER: US/08/556,978B
                                                                                  FILING DATE:
CLASSIFICATION: 435
PRIOR APPLICATION DATA:
APPLICATION NUMBER: 08/077,600
FILING DATE: JUNE 15, 1993
ATTORNEY/AGENT INFORMATION:
NAME: FLOYD, LINDA AXAMETHY
REGISTRATION NUMBER: 33,692
REPERENCE/POCKET VUMBER: CR-9389-A
TELEPHONE: 302-892-8112
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             ATTORNEY AGENT INFORMATION:
NAME: Granahan, Patricia
REGISTRATION NUMBER: 32,227
REFERENCE, DOCKET NUMBER: MIT-6141
TELECOMMUNICATION INFORMATION:
TELEPHONE: 617-861-6240
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     RESULT 11
US-08-068-747-1/c
Sequence 1, Application US/08068747
Patent No. 5695933
                                                                                                                                                                                                                                                                                                                                                 INFORMATION FOR SEQ 1D NO: 25: SEQUENCE CHARACTERISTICS: LENGTH: 93 base pairs TYPE: nucleic acid STRANDEDNESS: single
                                                                                                                                                                                                                                                                                                                                                                                                                                                                   TOPOLOGY: linear MOLECULE TYPE: DNA (genomic)
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SEQUENCE CHARACTER.STICS:
LENGTH: 51 base pairs
TYPE: nucleic acid
STRANDEDNESS: single
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               617-861-9540
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STATE: Massachusett
COUNTRY: USA
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        TELEPHONE:
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1210 CGGCAGCTGGAGCTGGAGAAGCAGCTGGAGAAGCAGCGGGAGCTGGAGCGGCAGC
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APPLICANT: Caceci, Thomas
APPLICANT: Caceci, Thomas
APPLICANT: Caceci, Thomas
APPLICANT: Caceci, Maria B.W.
TITLE OF INVENTION: SYNTHETIC ANTIFREEZE PEPTIDE AND
TITLE OF INVENTION: SYNTHETIC GENE CODING FOR ITS PRODUCTION
NUMBER OF SEQUENCES: 4
CORRESPONDENCE ADDRESS:
ADDRESSE: WHITHAM, CURTIS & WHITHAM
STREET: Suite 900
CITY: Reston
STREET: VA
COUNTRY: USA
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          0.8%; Score 29.4; DB 2; Length 57; 70.9%; Pred. No. 5.6e+02; tive 0; Mismatches 16; Indels
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         SOFTWARE: Patentin Release #1.0, Version #1.30
CURENT APPLICATION DATA:
APPLICATION NUMBER: US/07/814,220
FILING DATE: 23-DEC-1991
CLASSIFICATION 7435
PRIOR APPLICATION DATE:
APPLICATION NUMBER: US/07/88,437
FILING DATE: 25-SED-1990
ATTORNEY/AGENT INFORMATION:
NAWE: Whitham, Michael E.
REGISTRATION NUMBER: 32,635
                                                                                                                                                                                                                                                                                                                          MOLECULE TYPE: other nucleic acid
DESCRIPTION: /desc = "synthetic DNA"
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         MOLECULE TYPE: other nucleic acid
DESCRIPTION: /desc = "synthetic DNA"
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         REFERENCE/DOCKET NUMBER: 32,635
REFERENCE/DOCKET NUMBER: CIT.016
TELECOMMUNICATION INFORMATION:
TELEPHONE: 703-391-2510
TELEFRAX: 703-391-2510
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    ZIP: 20191
COMPUTER READABLE FORM:
MEDIUM TYPE: Floppy disk
COMPUTER: IBM PC compatible
OPERATING SYSTEM: PC-DOS/MS-DOS
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    Sequence 25, Application US/07814220 Patent No. 5925540
                  NAME: Whitham, Michael E.
REGIENTATION NUMBER: 32,635
REFERENCE/DOCKET NUMBER: CIT.
TELECOMMUNICATION INFORMATION:
TELEFRAM: 703-391-2510
TELEFRAM: 703-391-2510
INFORMATION FOR SEQ ID NO: 26: SEQUENCE CHARACTERISTICS:
LENGTH: 57 base pairs
TYRE: nucleic acid
STRAMBDNESS: double
ATTORNEY/AGENT INFORMATION:
                                                                                                                                                                                                                                                                                                                                                                                                                                                            Best Local Similarity 70.9
Matches 39; Conservative
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SEQUENCE CHARACTERISTICS:
LENGTH: 62 base pairs
TYPE: nucleic acid
STRANDEDNESS: double
                                                                                                                                                                                                                                                                                                          linear
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| Sequence 26, Application US/07812421
| Patent No. 5932697
| GENERAL INFORMATION:
| APPLICANT: Caccei, Thomas E. APPLICANT: Toth, Thomas E. APPLICANT: Szumanski, Maria B.W.
| TITLE OF INVENTION: SYNTHETIC ANTIFREEZE PEPTIDE AND TITLE OF INVENTION: SYNTHETIC GENE CODING FOR ITS PRODUCTION NUMBER OF SEQUENCES: 43
| CORRESPONDENCE ADDRESS: ADDRESSE: ANTITHAM CURIS & WHITHAM STREET: Reston Intl. Center, 11800 Sunrise Valley Dr., CTTW. Date: Soite 900
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               Query Match
0.8%; Score 29.4; DB 2; Length 57;
Best Local Similarity 70.9%; Pred. No. 5.6e+02;
Matches 39; Conservative 0; Mismatches 16; Indels
                                                                               COMPUTER READABLE FORM:

MEDIUM TYPE: Floppy disk
COMPUTER: IBM PC compatible
COMPUTER: TIBM PC compatible
COMPUTER: PatentIn Release #1.0, Version #1.30
CURRENT APPLICATION DATA:
APPLICATION NUMBER: US/07/814,220
FILING DATE: 23-DEC-1991
CLASSIFICATION DATA:
APPLICATION NUMBER: US 07/588,437
FILING DATE: 25-SEP-1990
ATTORNEY/AGENT INFORMATION:
NAME: Whitham, Michael E.
REGISTRATION NUMBER: 32,635
REGISTRATION INFORMATION:
TELEFHONE: 703-391-2510
TELEFRONE/COMPUTER: 703-391-2510
TELEFRONE CHARACTERISTICS:
LUNGTH: 57 DASS PARIE
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ZIP: 20191
COMPUTER READABLE FORM:
MEDIUM TYPE: Floppy disk
COMPUTER: IBM PC compatible
OPERATING SYSTEM: PC-DOS/MS-DOS
SOFTWARE: Patentin Release #1.0, Version #1.30
CURRENT APPLICATION DATA:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          other nucleic acid
/desc = "synthetic DNA"
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APPLICATION NUMBER: US 07/588,437
FILING DATE: 25-SEP-1990
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              APPLICATION NUMBER: US/07/812,421
FILING DATE: 23-DEC-1991
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  TYPE: nucleic acid
STRANDEDNESS: double
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       linear
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                                             USA
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      CITY: Reston
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    ; TOPOLOGY: 1i.
; MOLECULE TYPE:
; DESCRIPTION:
US-07-814-220-26
                                                                  20191
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US-07-812-421-26
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0; Gaps Query Match 0.8%; Score 29.4; DB 2; Length 62; Best Local Similarity 70.9%; Pred. No. 5.9e+02; Matches 39; Conservative 0; Mismatches 16; Indels

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Search completed: April 29, 2005, 02:23:45 Job time : 544.672 secs

Sequence

Sequence Sequence Sequence

J/, Appl J/, Appl Jequence 14338, A Sequence 157, Appl Sequence 21, Appl Sequence 14, Appl Sequence 14, Appl Sequence 14, Appl

...pl ...quence 14266, A Sequence 15706, A Sequence 15706, A Sequence 506

506, App 15, Appl 65, Appl 65, Appl 58, Appl

Sequence 15, 2 Sequence 65, 2 Sequence 65, 2

Searched:

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Title:

Database

Sequence 2343, Ap Sequence 66, Appl Sequence 66, Appl

Sequence 31, App.

Sequence

Sequence 11, Appl Sequence 14, Appl Sequence 14, Appl Sequence 65, Appl Sequence 22933, A Sequence 229, App Sequence 1351, App

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Gaps

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Length 60; Indels

Result

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US-09-908-975-10766

Sequence 10766, Application US/09908975

Sequence 10766, Application US/09908975

Sequence 10766, Application US/09908975

Sequence 10766, Application US/09908975

Sexure 10808AL INFORMATION: USED 10808-10808

APPLICANT: WINTZ, Eli
APPLICANT: WINTZ, Eli
APPLICANT: WINTZ, Eli
APPLICANT: MINTZ, Liat
APPLICANT: MINTZ, Liat
APPLICANT: MINTZ, Eli
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APPLICANT: MINTZ, Eli
APPLICANT: WINTZ, Eli
APPLICANT: WINTZ, Eli
APPLICANT: UNINTEN INAMBER: US/09/908,975

CURRENT APPLICATION NUMBER: US 60/221,607

PRIOR APPLICATION NUMBER: US 60/221,607

PRIOR APPLICATION NUMBER: US 60/221,607

PRIOR PILING DATE: 2000-07-28

NUMBER OF SEQ ID NOS: 32337

SOFTWARE: Patentin version 3.0

SEQ ID NO 10766
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       US-10-085-906-174
US-10-029-386-17340
US-10-029-386-17340
US-10-029-386-2222
US-09-373-658-52
US-09-989-687-52
US-10-029-386-687-52
US-10-029-386-687-57
US-10-021-323-14338
US-10-021-323-14266
US-10-021-323-14335
US-10-021-323-14335
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88.3%; Pred. No. 0.0022;
iive 0; Mismatches 7;
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US-10-021-323-14096
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US-09-922-261-229
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ORGANISM: Homo sapiens
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    Query Match
Best Local Similarity
Matches 53; Conserv
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Sequence 463, App
Sequence 6, Appli
Sequence 8, Appli
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Sequence 156, App
Sequence 462, App
Sequence 462, App
                                                                                                                                           April 28, 2005, 07:33:31 ; Search time 1939.12 Seconds (without alignments) 11433.739 Million cell updates/sec
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Sequence 339,
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(cgn2_6/ptodata/1/pubpna/US06_PUBW_PUB.seq:*
(cgn2_6/ptodata/1/pubpna/US06_PUBW_PUB.seq:*
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(cgn2_6/ptodata/1/pubpna/US06_PUBCOMB.seq:*
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                     GenCore version 5.1.6
Copyright (c) 1993 - 2005 Compugen Ltd.
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US-09-854-867-463

US-10-786-9078-463

US-10-313-894A-6

US-10-313-894A-6

US-10-30-864-761-24680

US-10-769-731-156

US-10-759-731-156

US-10-758-307-462

US-10-758-307-462

US-10-758-307-66
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Maximum Match 100%
Listing first 45 summaries
                                                                                                    OM nucleic - nucleic search, using sw model
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Gapop 10:0 , Gapext 1.0
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seq length: 100
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Match
                                                                                                                                                                                                                                                 Perfect score:
                                                                                                                                                                                                                                                                                                                 Scoring table:
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31.22
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Maximum DB
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ALIGNMENTS

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1192 CAGGAGCAGGAGGCCAAGCGGCAGCTGGAGCTGGAGAAGCAGCTGGAGAAGCAGCGGGAG 1251
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APPLICANT: RABBANI, ELAZAR
APPLICANT: STANTANOPOULOS, JANNIS G.
APPLICANT: DONEGAN, JAMES J.
TITLE OF INVENTION: MULTISIGNAL LABELING REAGENTS, AND PROCESSES AND USES
TITLE OF INVENTION: THEREFOR
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         1208 AGCGGCAGCTGGAGCTGGAGCAGCTGGAGAAGCAGCGGGAGCTGGAGCGGCAGC 1264
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        0; Gaps
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   Query Match
1.0%; Score 34.6; DB 18; Length 63;
Best Local Similarity 75.4%; Pred. No. 27;
Matches 43; Conservative 0; Mismatches 14; Indels
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         Length 87;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 Description of Combined DNA/RNA Molecule:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                OTHER INFORMATION: Description of Artificial Sequence:/note OTHER INFORMATION: synthetic construct
                                                                                                                                                                                                                               APPLICANT: Heing, Ann
TITLE OF INVENTION: METHODS AND COMPOSITIONS FOR PREDICTING
TITLE OF INVENTION: METHODS AND COMPOSITION FOR PREDICTING
FILE REPERENCE: 21108.0001U1
CURRENT PEPLICATION VUMBER: US/10/333,894A
CURRENT FILING DATE: 2003-01-24
NUMBER OF SEQ ID NOS: 21
SOFTWARE: FastSEQ for Windows Version 4.0
SEQ ID NO 6
LENGTH: 87
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        Indels
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    Query Match 1.0%; Score 36.6; DB 18;
Best Local Similarity 65.1%; Pred. No. 8.5;
Matches 54; Conservative 0; Mismatches 29;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   OTHER INFORMATION: Description of Combined DR OTHER INFORMATION: Synthetic oligonucleotide
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             FILE REFERENCE: ENZ-65
CURRENT APPLICATION NUMBER: US/10/407,818
CURRENT FILING DATE: 2003-04-03
NUMBER OF SEQ ID NOS: 16
SOFTWARE: PATENTIN Ver. 2.1
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   1252 CTGGAGCGCAGCGAGAGGAGGA 1274
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    64 cagciacacidedacacide 86
                                                                                                                         Sequence 6, Application US/10333894A
Publication No. US20040259085A1
GENERAL INFORMATION:
APPLICANT: Chang, Chammehang
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 Sequence 8, Application US/10407818
Publication No. US20040198971A1
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                TYPE: DNA
ORGANISM: Artificial Sequence
FEATURE:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            ORGANISM: Artificial Sequence
61 GCAGCAGC 68
                                                                       RESULT 4
US-10-333-894A-6
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       US-10-333-894A-6
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        TYPE: DNA
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Sequence 463, Application US/10786970A

Publication No. US2005064449A1

GENERAL INFORMATION:

APPLICANT: JOAN, FULL

APPLICANT: JOAN, FULL

APPLICANT: JOAN, PETER

TITLE OF INVENTION: SINGLE COPY GENOMIC HYBRIDIZATION PROBES AND METHOD OF GENERATING FILE REFERENCE: 30307

CURRENT APPLICATION NUMBER: US/10/786,970A

CURRENT FILING DATE: 2004-02-24

PRIOR APPLICATION NUMBER: US/09/573,080

PRIOR PETING DATE: 2000-05-16

NUMBER OF SEQ ID NOS: 479

SEQ ID NO 463

LENGTH: 69
                                                                                                                                                             APPLICANT: JOAN, KNOLL H
APPLICANT: JOAN, KNOLL H
APPLICANT: GOGAN, PETER K
TITLE OF INVENTION: SINGLE COPY GENOMIC HYBRIDIZATION PROBES AND METHOD OF GENERATING
FILE REFERENCE: 30307, 10309/854,867
CURRENT APPLICATION NUMBER: US/09/854,867
CURRENT FILING DATE: 2003-05-08
NUMBER OF SEQ ID NOS: 613
SOFTWARE: PATENTIN Version 3.1
SEQ ID NO 463
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             OTHER INFORMATION: Description of Artificial Sequence: repetitive sequence found in CATHER INFORMATION: many eutherial genomes. Length of core repeating element is vari; OTHER INFORMATION: able and is often polymorphi
US-10-786-9708A-463
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              OTHER INFORMATION: Description of Artificial Sequence: repetitive sequence found in OTHER INFORMATION: many eutherial genomes. Length of core repeating element is vari OTHER INFORMATION: able and is often polymorphic
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Best Local Similarity 72.1%; Pred. No. 3.9;
Matches 49; Conservative 0; Mismatches 19; Indels
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                                                                                                   Sequence 463, Application US/09854867
Publication No. US20030224356A1
GENERAL INFORMATION:
                                                                                                                                                                                                                                                                                                                                                                                                                                                         TYPE: DNA ORGANISM: Artificial Sequence
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               Query Match 1.0%;
Best Local Similarity 72.1%;
Matches 49; Conservative
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 RESULT 3
US-10-786-970A-463
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 US-09-854-867-463
                                                                                                                                                                                                                                                                                                                                                                                                                              LENGTH: 69
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1210 CGGCAGCTGGAGCTGGAGAAGCAGCTGGAGAAGCAGCGGGAGCTGGAGCGGCAGCGAGAA 1268
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                                        Query Match
0.9%; Score 33.4; DB 9; Length 93;
Best Local Similarity 72.9%; Pred. No. 73;
Matches 43; Conservative 0; Mismatches 16; Indels
                                                                                                                                                                                                                                                                                                                          Sequence 156, Application US/10759731A

Sequence 156, Application US/10759731A

PUBLICALION NO. US20050079574A1

GENERAL INFORMATION:

APPLICANT: Bond, Christoper J.

TITLE OF INVENTION: SYNTHETIC ANTIBODY PHAGE LIBRARIES

TITLE OF INVENTION: SYNTHETIC ANTIBODY PHAGE LIBRARIES

TITLE OF INVENTION SYNTHETIC ANTIBODY PHAGE LIBRARIES

CURRENT APPLICATION NUMBER: US/10/759, 731A

PRIOR PILING DATE: 2003-01-16

PRIOR PILING DATE: 2003-01-16

PRIOR APPLICATION NUMBER: US 60/488,610

PRIOR PILING DATE: 2003-01-16

PRIOR PILING DATE: 2003-01-16

PRIOR PILING DATE: 2003-10-08

NUMBER OF SEQ ID NOS: 194

SOFTWARE: PALENTIN VERSION 3.3

SEQ ID NO 156
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NAME/KEY: misc feature
LOCATION: (26)...(26)
OTHER INFORMATION: y is c or t
FEATURE:
NAME/KEY: misc feature
LOCATION: (28)...(28)
OTHER INFORMATION: s is g or c
FEATURE:
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LOCATION: (43)...(43)
OTHER INFORMATION: k is g or t
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LOCATION: (29)...(29)
OTHER INFORMATION: y is c or t
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LOCATION: (37)...(38)
OTHER INFORMATION: s is g or c
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ORGANISM: Artificial Sequence
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LOCATION: (34)...(35)
OTHER INFORMATION: 8 is
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OTHER INFORMATION: 8 is
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OTHER INFORMATION: r is
FEATURE:
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OTHER INFORMATION: m is
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NAME/KEY: misc feature
LOCATION: (46)..(46)
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                                                                                                                                                                                                           PRICEAR NO. USO2020044763A1

APPLICANT: Rank, baried R.
APPLICANT: Chen, Wenneheng
ITILE OF INVENTION: HAMMA GENOME-DERIVED SINGLE EXON NUCLEIC ACID PROBES USEFUL FOR ITILE OF INVENTION: HAMMA GENOME-DERIVED SINGLE EXON NUCLEIC ACID PROBES USEFUL FOR ITILE OF INVENTION: HAMMA GENOME-DERIVED SINGLE EXON NUCLEIC ACID PROBES USEFUL FOR STATE OF INVENTION: HAMMA GENOME-DERIVED SINGLE EXON NUCLEIC ACID FORDER TILE OF INVENTION: HAMMA GENOME-DERIVED SINGLE EXON NUCLEIC ACID FORDER TILE OF INVENTION: HAMMA GENOME-DERIVED SINGLE EXON NUCLEIC ACID FORDER TILE OF INVENTION NUMBER: US 09/632,366

PRIOR FILING DATE: 2001-05-20

PRIOR PELICATION NUMBER: PC/USO1/0666

PRIOR PLICATION NUMBER: PC/USO1/0667

PRIOR PLICATION NUMBER: PC/USO1/0667
N: EXPRESSED IN LUNG, SIGNAL = 2.8

N: EXPRESSED IN PLACENTA, SIGNAL = 2.4

N: EXPRESSED IN ADULT LIVER, SIGNAL = 1.9

N: EXPRESSED IN HELA, SIGNAL = 3.5

N: EXPRESSED IN HELA, SIGNAL = 3.9

N: EXPRESSED IN HEARIN, SIGNAL = 4.5

N: EXPRESSED IN HEARIN, SIGNAL = 4.6

N: EXPRESSED IN FETAL LIVER, SIGNAL = 4.6

N: NT HIT: 415031896, EVALUE 2.000-13

N: EST_HUMAN HIT: R18580.1, EVALUE 3.000-13
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SOFTWARE: Annomax Sequence Listing Engine vers. 1.1
                                                                                                                                                                               ; Sequence 24680, Application US/09864761
; Patent No. US20020048763A1
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ORGANISM: Homo sapiens
FEATURE:
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LENGTH: 93
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Sequence 462, Application US/10786970A

Publication No. US20050064449A1

GENERAL INFORMATION:

APPLICANT: JOAN, KNOLL

APPLICANT: ROGAN, PETER

TITLE OF INVENTION: SINGLE COPY GENOMIC HYBRIDIZATION PROBES AND METHOD OF GENERATING CURRENT APPLICATION NUMBER: US/10/786,970A

CURRENT FILING DATE: 2004-02-24

PRIOR PAPLICATION NUMBER: US/99/573,080

PRIOR FILING DATE: 2000-05-16

NUMBER OF SEQ ID NOS: 479

SEQ ID NO 462

LENGTH: 69
                                                                                                                                                                                            OTHER INFORMATION: Description of Artificial Sequence: repetitive sequence found in OTHER INFORMATION: many eutherial genomes. Length of core repeating element is varia; OTHER INFORMATION: ble and is often polymorphic US-09-854-867-462
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       OTHER INFORMATION: Description of Artificial Sequence: repetitive sequence found in OTHER INFORMATION: many eutherial genomes. Length of core repeating element is varia; OTHER INFORMATION: ble and is often polymorphi
US-10-786-970A-462
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               ,°
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0
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Best Local Similarity 66.7%; Pred. No. 1.4e+02;
Matches 46; Conservative 0; Mismatches 23;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            US-10-758-307-66
; Sequence 66, Application US/10758307
; Publication No. US2004029290A1
; GENERAL INFORMATION:
APPLICANT: GENOMIC HEALTH, INC.
; APPLICANT: RUSH UNIVERSITY MEDICAL CENTER
; APPLICANT: Cobleigh, Melody
CURRENT APPLICATION NUMBER: US/09/854,867
CURRENT FILING DATE: 2003-05-08
NUMBER OF SEQ ID NOS: 613
SOFTWARE: Patentin version 3.1
SEQ ID NO 462
                                                                                                                                                     ORGANISM: Artificial Sequence
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                                                                                                                                                                                                                                                                                                           Query Match
Best Local Similarity
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                                                                                                               LENGTH: 69
                                                                                                                                   TYPE: DNA
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Publication No. US20030224356A1

GENERAL INFORMATION:

APPLICANT: ROGAN, KNOLL H

APPLICANT: ROGAN, PETER K

TITLE OF INVENTION: SINGLE COPY GENOMIC HYBRIDIZATION PROBES AND METHOD OF GENERATING

FILE REFERENCE: 30307
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            1196 AGCAGGAGGCCAAGCGGCAGCTGGAGCTGGAGAAGCAGCTGGAGAAGCAGCGGGAGCTGG 1255
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                1256 AGCGCCAGCGAGAGGAGGAGGAGG 1281
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; OTHER INFORMATION: k is g or t
US-10-759-731A-156
                                                                                                                                                                                                                                             OCATION: (55)...., (55) , , )
)THER INFORMATION: r is a or g
                                                                                                                                                                                                                                                                                                                                    NAME/KEY: misc feature
LOCATION: (59)...(59)
THER INFORMATION: y is c or
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OTHER INFORMATION: y is c or
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THER INFORMATION: 8 18 g or
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OTHER INFORMATION: m is a or
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                                                                   JOCATION: (50)...(50)
THER INFORMATION: Y is
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THER INFORMATION: 8 is
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LOCATION: (58)...(58)
OTHER INFORMATION: k is
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THER INFORMATION: r is
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THER INFORMATION: 8 is
    OTHER INFORMATION: k is
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LOCATION: (68)...(68)
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                                           NAME/KEY: misc feature
LOCATION: (50)..(50)
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Best Local Similarity
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US-09-854-867-462
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Matches
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Query Match
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| Sequence 339, Application US/10852797
| Publication No. US20050064455A1
| GENERAL INFORMATION:
| APPLICANT: Genomic Health, Inc. |
| APPLICANT: Baker, Joffre |
| APPLICANT: Baker, Joffre |
| APPLICANT: Shak, Steven |
| APPLICANT: Sledge, George |
| APPLICANT: Sledge, George |
| APPLICANT: Soule, Sharon |
| TITLE OF INVENTION: Response to Chemotherapy |
| TITLE OF INVENTION: NUMBER: 60/473,970 |
| PRIOR PILING DATE: 2003-05-24 |
| PRIOR PILING DATE: 2003-05-28 |
| NUMBER OF SEQ ID NOS: 372 |
| SOFTWARE: FREESE for Mindows Version 4.0
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            Length 77;
                                                                                                                                                                                                                                                                                                                                                                                                                                                               Score 31.2; DB 18; Length 77;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               Indels
          TITLE OF INVENTION: GENE EXPRESSION MARKERS FOR BREAST
TITLE OF INVENTION: GENE EXPRESSION MARKERS FOR BREAST
TITLE OF INVENTION: CANCER PROGNOSIS
FILE REFERENCE: 3940/0008 US
CURRENT APPLICATION NUMBER: US 10/10/758,307
CURRENT FILING DATE: 2004-01-14
FRIOR FILING DATE: 2003-01-15
NUMBER OF SEQ ID NOS: 440
SOFTWARE FEASES FOR Windows Version 4.0
SEQ ID NO 66
LENGTH: 77
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            DB 19;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       .8e+02;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     .8e+02;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  0; Mismatches
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  0; Mismatches
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            Score 31.2;
Pred. No. 2.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            Sequence 174, Application US/10085906 Publication No. US20030054371A1 GENERAL INFORMATION:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          Pred.
                                                                                                                                                                                                                                                                                                  TYPE: DNA
ORGANISM: Artificial Sequence
                                                                                                                                                                                                                                                                                                                                                                                                                                                             0.9%;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  TYPE: DNA
ORGANISM: Artificial Sequence
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          Query Match 0.9%;
Best Local Similarity 70.0%;
Matches 42; Conservative
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       FEATURE:
COTHER INFORMATION: amplicon
US-10-852-797-339
                                                                                                                                                                                                                                                                                                                                                          FEATURE: OTHER INFORMATION: Amplicon
Cronin, Maureen
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     Best Local Similarity 70.0
Matches 42; Conservative
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         APPLICANT: Ying, Vincent APPLICANT: Wu, Paul
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    US-10-085-906-174/c
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               RESULT 11
US-10-852-797-339
                                                                                                                                                                                                                                                                                                                                                                                                             US-10-758-307-66
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                  Query Match
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Sequence 17340, Application US/10029386
Publication No. US20030194704A1
GENERAL INFORMATION:
APPLICANT: Ranh, David R.
APPLICANT: Hanzel, David R.
APPLICANT: Hanzel, David R.
TITLE OF INVENTION: EXPRESSION ANALYSIS TWO
FILE REPERBNCE: AEOMICA-X-2
CURRENT APPLICATION NUMBER: US/10/029,386
CURRENT FILING DATE: 2001-12-20
NUMBER OF SEQ ID NOS: 34288
SOFTWARE: Annomax Sequence Listing Engine vers. 1.1
SEQ ID NO 17340
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 1169 AGGAGAGGAAAGAGCGGGAGCGCCAGGAGCAGCCCAAGCGGCAGCTGGAGCTGGAGA 1228
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                0; Gaps
APPLICANT: Gray, Gary S.
TITLE OF INVENTION: POLYMORPHIC ELEMENTS IN THE
TITLE OF INVENTION: COSTIMULATORY RECEPTOR LOCUS AND USES THEREOF
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          Score 30.8; DB 16; Length 99;
Pred. No. 4.2e+02;
0; Mismatches 27; Indels
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  DB 14; Length 86;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         OTHER INFORMATION: MAP TO AL135920.4

OTHER INFORMATION: EXPRESSED IN BONE MARROW, SIGNAL = 8.7

OTHER INFORMATION: EXPRESSED IN HELA, SIGNAL = 3.5

OTHER INFORMATION: EXPRESSED IN FETAL LIVER, SIGNAL = 13

OTHER INFORMATION: EXPRESSED IN HEART, SIGNAL = 8

OTHER INFORMATION: HIT: D86240.2, EVALUE 4.90e+00
US-10-029-386-17340
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     3e+02;
33;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 0; Mismatches
                                                             TILE REPERENCE: GNN-5543CP2
CURRENT APPLICATION NUMBER: US/10/085,906
CURRENT FILIND DATE: 2002-02-27
PRIOR APPLICATION NUMBER: US 60/126,215
PRIOR FILING DATE: 1999-03-25
PRIOR FILING DATE: 2000-03-24
PRIOR FILING DATE: 2000-03-24
PRIOR PILING DATE: 2000-03-24
PRIOR PILING DATE: 2000-03-24
NUMBER OF SEQ ID NOS: 545
SOFTWARE: PSECSEQ for Windows Version 4.0
SSOFTWARE: P86
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  0.9%; Score 31.2;
60.7%; Pred. No. 3e-
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   1279 AGGAAGGAGATCGAGAGGCGCGAG 1302
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 25 AAGGGAGAGAGGGAGAGGGAGAG
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        ocn 0.8%; 1 Similarity 63.5%; 47; Conservative
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       Best Local Similarity 60.7
Matches 51; Conservative
                                                                                                                                                                                                                                                                                                                                                                                              ; TYPE: DNA; ORGANISM: Homo sapiens
US-10-085-906-174
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    TYPE: DNA
ORGANISM: Homo sapiens
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             Query Match
Best Local Similarity
Matches 47; Conserv
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RESULT 14
US-10-159-71A-155/C

Sequence 155, Application US/10759731A

Publication No. US20050079574A1

GENERAL INFORMATION:
TITLE OF INVENTION: SYNTHETIC ANTIBODY PHAGE LIBRARIES
FILE REFRENCE: 11669.136USUJ

CURRENT FILING DATE: 2004-01-16

PRIOR APPLICATION NUMBER: US 60/441,059

PRIOR APPLICATION NUMBER: US 60/441,059

PRIOR APPLICATION NUMBER: US 60/486,610

PRIOR PILING DATE: 2003-01-16

PRIOR PILING DATE: 2003-01-16

PRIOR FILING DATE: 2003-01-16

PRIOR FILING DATE: 2003-01-16

PRIOR FILING DATE: 2003-10-08

NUMBER OF SEQ ID NOS: 194

SEQ ID NO 155

LENGTH: 87
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    OTHER INFORMATION: RIG ala scan
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 FEATURE:
NAME/KEY: misc_feature
LOCATION: (32) .. (32)
OTHER INFORMATION: s is g or c
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      FEATURE:
NAME/KRY: misc_feature
LOCATION: (34)...(35)
OTHER INFORMATION: s is g or c
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LOCATION: (49)...(49)
OTHER INFORMATION: s is g or c
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LOCATION: (37)...(37)
OTHER INFORMATION: k is g or t
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THER INFORMATION: y is c or t
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THER INFORMATION: m is a or c
                                                                                                                                                                                                                                                                                                                                                                                                                                      TYPE: DNA
ORGANISM: Artificial Sequence
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LOCATION: (25)...(26)
OTHER INFORMATION: s is g or
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LOCATION: (43)...(43)
OTHER INFORMATION: k is g or
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LOCATION: (44)...(44)
OTHER INFORMATION: y is c
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THER INFORMATION: y is c
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LOCATION: (28)...(28)
OTHER INFORMATION: r is
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OTHER INFORMATION: r is
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NAME/KEY: misc_feature
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1196 AGCAGGAGGCCAAGCGGCAGCTGGAGCTGGAGAAGCAGCTGGAGAAGCAGCGGGAGCTGG 1255
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0.8%; Score 30.4; DB 19;
Best Local Similarity 39.5%; Pred. No. 5.1e+02;
Matches 34; Conservative 23; Mismatches 29;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              Sequence 11, Application US/10061201
Publication No. US2030166229A1
GENERAL INFORMATION:
APPLICANT: Shamon, Mark
TITLE OF INVENTION: HUMAN POSH-LIKE PROTEIN 1
FILE REFERENCE: PB0178
CURRENT APPLICATION NUMBER: US/10/061,201
CURRENT FILING DATE: 2002-01-30
PRIOR PLILING DATE: 2001-01-30
PRIOR APPLICATION NUMBER: PCT/US01/00666
PRIOR APPLICATION NUMBER: PCT/US01/00667
PRIOR FILING DATE: 2001-01-30
PRIOR FILING DATE: 2001-01-30
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               1256 AGCGCCAGCGAGAGGAGGAGGAGG 1281
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                                                                                 NAME/KEY: misc feature
LOCATION: (52)...(53)
OTHER INFORMATION: 8 is g or c
                                                                                                                                                                                                                                                                                                                                                NAME/KEY: misc feature
LOCATION: (61)...(61)
OTHER INFORMATION: k is g or t
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NAME/KRX: misc feature
LOCATION: (65)-.(65)
OTHER INFORMATION: s is g or c
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  NAME/KEY: misc feature
LOCATION: (70)...(70)
OTHER INFORMATION: r is a or g
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 ; OTHER INFORMATION: S iS G Or C US-10-759-731A-155
                      LOCATION: (50)...(50)
OTHER INFORMATION: y is c or t
                                                                                                                                                                                                 LOCATION: (55)..(56)
OTHER INFORMATION: s is g or c
                                                                                                                                                                                                                                                                                                                                                                                                                                    NAME/KEY: misc feature
LOCATION: (64)...(64)
OTHER INFORMATION: k is g or t
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     LOCATION: (68)...(68)
OTHER INFORMATION: y is c or t
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      NAME/KEY: misc feature
LOCATION: (73)...(73)
OTHER INFORMATION: k is g
                                                                                                                                                                                                                                                                                  FEATURE:
NAME/KEY: misc feature
LOCATION: (74)...(74)
                                                                                                                                                                     NAME/KEY: misc_feature
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WAME/KEY: misc feature
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US-10-061-201-11
                                                                                                                                                                                            LOCATION:
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Score 30.4; DB 16; Length 96;
Pred. No. 5.4e+02;
0; Mismatches 41; Indels
                                              PRIOR APPLICATION NUMBER: PCT/USO1/00669
PRIOR FILING DATE: 2001-01-30
PRIOR APPLICATION NUMBER: PCT/USO1/00665
PRIOR APPLICATION NUMBER: PCT/USO1/00666
PRIOR APPLICATION NUMBER: PCT/USO1/00668
PRIOR PILING DATE: 2001-01-30
PRIOR PILING DATE: 2001-10-10
NUMBER OF SEQ ID NOS: 4162
SOFTWARE: Aeomica Sequence Listing Engine
SEG ID NO 11
APPLICATION NUMBER: PCT/US01/00664
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          Query Match 0.8%;
Best Local Similarity 57.3%;
Matches 55; Conservative (
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            TYPE: DNA
CORGANISM: Homo sapiens
US-10-061-201-11
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3574 GGGCAAGTTGGGCTCTTCCCATCCAATTATGTAAAG 3609 61 GATAAAGTAGCATCTTCCCTATCTTGTTGTAGAG 96 ò

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Gaps

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Search completed: April 29, 2005, 03:41:19 Job time : 1940.12 secs

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Sequence:

Searched:

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PAT 30-JAN-2004
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AY233993 Arabidops
AX921455 Sequence
BD117008 EST and e
AX107476 Sequence
CQ542573 Sequence
CQ538403 Sequence
CQ725585 Sequence
AY045524 Panthera
AY104049 Drosophil
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AY293992 Arabidops
A43830 Sequence 4
II7407 Sequence 4
BD270475 Synthetic
AX039308 Sequence
AX039517 Sequence
                                                                                      AY293995 Arabidops
AY29394 Arabidops
AY29394 Arabidops
AX530502 Sequence
AY184037 Drosophil
AY184053 Drosophil
AY184051 Drosophil
AY132812 Femerope
AX902306 Sequence
BD037839 Sequence
                                                                                                   Arabidops
Arabidops
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Fennerope
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Drosophil
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Mammalia; Butheria; Primates; Catarrhini; Hominidae; Homo.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   1
Shoshan, A., Wasserman, A., Mintz, E., Mintz, L. and Faigler, S.
Oligonucleotide library for detecting rna transcripts and splice
variants that populate a transcriptone
Patent: WO 0210449-A 10766 07-FEB-2002;
Compugen Inc. (US)
Location/Qualifiers
                      Drosophil
                                  Drosophil
                                                                 Cladobotry
                                                                               Fennerope
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Ditylum
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          AY184035 I
AY184060 I
AY184027 I
AY184026 I
AY545903 I
Y17097 CL2
AY545901 I
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 Length:
Matches:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        /mol_type="unassigned DNA"
/db_xref="taxon:9606"
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  ALIGNMENTS
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  1. .60
/organism="Homo sapiens"
                                                                                                                                                                                                                  MMVIMV30
AY293993
          AY184035
AY184060
AY184027
AY184026
AY545903
CMY17097
                                                                                                                          AX530502
AY184038
AY184047
AY184053
AY184051
AY132812
AX32812
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AY295846
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AY295845
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AY045524
AY184049
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AX039517
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I17407
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102.00
100.00$
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                                                                                                  70.5
67.5
67.5
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        DEFINITION
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AUTHORS
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-MODEL=frame+ p2n. model -DEV=xlh
-MODEL=frame+ p2n. model -DEV=xlh
-Q=/cgn2_1/USPTO_spool/US09674237/runat_27042005_182121_2876/app_query.fasta_1.1351
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-DB=GenEmb1 -QFWT=fastap -SUFFTX=szlm100_rge -MINMATCH=0.1 -LOOPCL=0
-LOOPEXT=0 -UNITS=bits -START=1 -END=-1 -MATRIX=blosum62 -TRANS=human40.cdi
-LIST=45 -DOCALIGN=200 -THR SCORE==ptt -THR MAX=100 -THR MIN-6 -ALIGN=15
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-USER=US09674237_@CGN 1 1 7319 @runat_27042005_182121_2876 -NCPU=6 -ICPU=3
-NO MAAP -LARGEQUERY -NGG_SCORES=0 -WAIT -DSPEDCCK=100 -LONGLOG
-DBV_TIMEOUT=120 -WARN TIMEOUT=30 -THREADS=1 -XGARDOP=10 -XGAREXT=0.5 -FGAPOP=6
-FGAPOR=17 -YGAPOP=10 -YGAPEXT=0.5 -DELOP=6 -DELEXT=7
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   CQ541131 Sequence
AR208350 Sequence
AR208351 Sequence
AY545898 Fennerope
                                                                                       (without alignments)
4849.920 Million cell updates/sec
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.
                                                                                                                                              MAQPPTPFGGSLDVWAITVE.....VGLFPSNYVKLTTDMDPSQQ 1213
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                                                                           April 28, 2005, 21:36:20 ; Search time 12119 Seconds
                                                                                                                                                                                                                                                                2238514
         GenCore version 5.1.6
Copyright (c) 1993 - 2005 Compugen Ltd.
                                                    nucleic search, using frame_plus_p2n model
                                                                                                                                                                                                                                        4708233 seqs, 24227607955 residues
                                                                                                                                                                                                                                                            Total number of hits satisfying chosen parameters:
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Listing first 45 summaries
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/rpt_type=tandem
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Fenneropenaeus chinensis
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Dawkins, R. Lettes. and Abraham, L. Joseph.
Method for determining ancestral haplotypes using haplospecific geometric elements within the major histocompatibility complex multigene cluster
Patent: US 633747-A 7 07-MAY-2002;
Location/Qualifiers
                                                                                                                                                                                                                                                    (bases 1 to 96)
Dawkins, R.Letts. and Abraham, L.Joseph:
Method for determining ancestral haplotypes using haplospecific geometric elements within the major histocompatibility complex multigene cluster
Patent: US 633747-A 6 07-WAY-2002;
Location/Qualifiers
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/wol_type="unassigned DNA"
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6383747.
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                                                   (1-60)
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/organism="unknown"
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Sequence 6 from patent US
AR208350
AR208350.1 GI:21509481
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98 bp DNA linear INV 08-MAR-2004
Fenneropenaeus chinensis clone TE1-122696 microsatellite sequence.
AY545898
AY545898.1 GI:44894761
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                                                                                                                                                                                      DNA
                                                                                                                                                                                                                                                                                                                                                                                                                                                                            Eukaryota; Metazoa; Arthropoda; Crustacea; Malacostraca;
Eumalacostraca; Eucarida; Decapoda; Dendrobranchiata; Penaeoidea;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       Z (bases 1 to 98)

Kong, J., Meng, X., Liu, P. and Gao, H.

Direct Submission

Submitted (07-FEB-2004) Germplasm Resources and Genetic Breeding
Laboratory, Yellow Sea Fisheries Research Institute, 106 Nanjing
Road, Qingdao, Shandong 266071, P. R. China
Location/Qualifiers
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           Penaeidae, Fenneropenaeus.

1 (bases 1 to 98)
Kong, J., Meng, X., Liu, P. and Gao, H.
Selection of polymorphic microsatellites from random shearing lunpublished
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/note="microsatellite"
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                                                                                                                    Rynearson, T.A. and Armbrust, E.V.
Rynearson, T.A. and Armbrust, E.V.
DNA fingerprinting reveals extensive genetic diversity in a field population of the centric diatom Ditylum brightwellii
Limnol. Oceanogr. 45 (6), 1329-1340 (2000)
Limnol. Oceanogr. 45 (6), 1329-1340 (2000)

Rynearson, T.A. and Armbrust, E.V.
Direct Submission
Submitted (03-MAY-2000) Oceanography, University of Washington, Box 357940, Seattle, WA 98195, USA
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         AY184035 99 bp DNA linear INV 27-FEB-2003
Drosophila melanogaster clone TTCTC28 centromeric satellite
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                                                                                                                                                                                                                                                                                                                                             /mol_type="genomic Dark"
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/isolation_source="Ditylum brightwellii, clone CCMP 358;
/center for the Culture of Marine Phytoplankton"
/db xref="taxon:49249"
/clone="Dbr2"
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      Submitted (20-NOV-2002) MCBL, The Salk Institute, 10010 N. Torrey Pines Rd., La Jolla, CA 92037, USA
                                                                                      Bacillariophyta; Coscinodiscophyceae;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           Drosophila melanogaster (fruit fly)
Drosophila melanogaster
Bukaryota, Metazoa, Arthropoda; Hexapoda; Insecta; Pterygota;
Bukaryota, Edopterary Brachycera; Muscomorpha;
Ephydroidea; Drosophilidae; Drosophila.
1 (bases 1 to 99)
Sun, X., Le, H.D., Wahlstrom, J.M. and Karpen, G.H.
Sequence analysis of a functional Drosophila centromere
Genome Res. 13 (2), 182-194 (2003)
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        2 '(bases 1 to 99)
Sun,X., Le,H.D., Wahlstrom,J.M. and Karpen,G.H.
Direct Submission
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/mol type="genomic DNA"
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/rpt_type=tandem
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                                                                                      Bukaryota; stramenopiles;
Lithodesmiaceae; Ditylum.
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AY184035.1 GI:28193785
                     GI:9802316
                                                     Ditylum brightwellii
                                                                       Ditylum brightwellii
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AY184060 99 bp DNA linear INV 27-FEB-2003
Drosophila melanogaster clone TTCTC53 centromeric satellite
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         Bukaryota; Metazoa; Arthropoda; Hexapoda; Insecta; Pterygota; Neoptera; Bndopterygota; Diptera; Brachycera; Muscomorpha; Ephydroidea; Drosophilidae; Drosophila
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       Sun,X., Le,H.D., Wahlstrom,J.M. and Karpen,G.H.
Sequence analysis of a functional Drosophila centromere
Genome Res. 13 (2), 182-194 (2003)
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Sun,X., Le,H.D., Wahlstrom,J.M. and Karpen,G.H.
Direct Submission
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                                          melanogaster"
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Matches:
Conservative:
Mismatches:
Indels:
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Drosophila melanogaster
                                     /organism="Drosophila mel/mol_type="genomic DNA"
db_xref="taxon:7227"
/map="centromere"
/clone="TTCTC28"
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Location/Qualifiers
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/note="satellite"
/rpt_type=tandem
/rpt_unit="ttctc"
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/note="satellite"
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/rpt_unit="ttctc"
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AY184060.1 GI:28193810
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75.50
68.29%
39.02%
1.20%
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Best Local Similarity:
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Drosophila melanogaster clone TTCTC20 centromeric satellite
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2. (bases 1 to 100)
Sun,X., Le,H.D., Wahlstrom,J.M. and Karpen,G.H.
Direct Submission
Submitted (20-000-2002) MCBL, The Salk Institute, 10010 N. Torrey
Pines Rd., La Jolla, CA 92017, USA
Location/Qualifiers
                                                                                                                                                                         64
                                                                                                                                                                                                                  Drosophila melanogaster (fruit fly)
Drosophila melanogaster
Eukaryota, Metazoa, Arthropoda; Hexapoda; Insecta; Pterygota;
Mospera; Endopterrygota; Diptera; Brachycera; Muscomorpha;
Ephydroidea; Drosophilidae; Drosophila.

1 (bases 1 to 100)
Sun,X., Le,H.D., Wahlstrom,J.M. and Karpen,G.H.
Sequence analysis of a functional Drosophila centromere
Genome Res. 13 (2), 182-194 (2003)
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/organism="Drosophila melanogaster"
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/db_xref="taxon:7227"
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/note="satellite"
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/rpt_unit="ttctc"
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389 GluGlnGluArgLysGluArgGluArgGlnGluGlnGluAlaLysArgGlnLeuGluLeu 408

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AY184026 10V 27-FEB-2003
Drosophila melanogaster clone TTCTC19 centromeric satellite
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                                      409 GluLysGlnLeuGluLysGlnArgGluLeuGluArgGlnArgGluGluGluArgArgLys 428
64
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Direct Submission
Submitted (20-NOV-2002) MCBL, The Salk Institute, 10010 N. Torrey
Pines Rd., La Jolla, CA 92037, USA
Location/Qualifiers
                                                                            Drosophila melanogaster

Bukaryota; Metazoa; Arthropoda; Hexapoda; Insecta; Pterygo
Neoptera; Endopterygota; Diptera; Brachycera; Muscomorpha;
Ephydroidea; Drosophilidae; Drosophila.

1 (bases 1 to 99)
Sun,X., Le,H.D., Wahlstrom,J.M. and Karpen,G.H.
Sequence analysis of a functional Drosophila centromere
Genome Res. 13 (2), 182-194 (2003)
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/note="Batellite"
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/rpt_unit="ttctc"
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74.50
66.67%
38.10%
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Genetic and morphological characterization of Cladobotryum species
causing cobweb disease of mushrooms
Appl. Environ. Microbiol. 65 (2), 606-610 (1999)
99124595
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                415 GlnArgGluLeuGluArgGlnArgGluGluGluArgArgLysGluIleGluArgArgGlu 434
                                                                                                                                                                  Kong, J., Meng, X., Liu, P. and Gao, H.
Selection of polymorphic microsatellites from random shearing DNA
clones in Fenneropenaeus chinensis
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 43
                                                                                  Fenneropenaeus chinensis
Bukaryota; Metazoa; Arthropoda; Crustacea; Malacostraca;
Eumalacostraca; Eucarida; Decapoda; Dendrobranchiata; Penaeoidea;
Penaeidae; Fenneropenaeus.
1 (bases 1 to 90)
Fenneropenaeus chinensis clone TE4-43565 microsatellite sequence.
AYS45903
                                                                                                                                                                                                                                                                                Submitted (07-FEB-2004) Germplasm Resources and Genetic Breeding Laboratory, Fallow Sea Fisheries Research Institute, 106 Nanjing Road, Qingdao, Shandong 266071, P. R. China Location/Qualifiers
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    Submitted (01-APR-1998) G.J. McKay, Queens University Belfast, Department of Applied Plant Science, Newforge Lane, Belfast, N. Ireland BT9 5PX, UK
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               Eukaryota; Fungi; Ascomycota; Pezizomycotina; Sordariomycetes;
Hypocreomycetidae; Hypocreales; Hypocreaceae; Hypomyces.
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/mol type="genomic DNA"
/db xref="taxon:139456"
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Mismatches:
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Matches:
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Direct Submission
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/note="microsatellite"
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                                                                     Fenneropenaeus chinensis
                                     AY545903.1 GI:44894766
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44.44%
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Hypomyces odoratus
Hypomyces odoratus
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AUTHORS
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INV 08-MAR-2004
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                                                                                                                                                                                                                                                                                                                                                                                    98 bp DNA linear INV 08-WAR-20.
AY545901
AY545901.1 GI:44894764
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      Kong,J., Meng,X., Liu,P. and Gao,H.
Selection of polymorphic microsatellites from random shearing DNA
clones in Fenneropenaeus chinensis
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    Fenneropenaeus chinensis
Eukaryota, Metazoa, Arthropoda, Crustacea, Malacostraca,
Eumalacostraca, Bucarida, Decapoda, Dendrobranchiata, Penaeoidea,
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      Submitted (07-FEB-2004) Germplasm Resources and Genetic Breeding Laboratory, Yellow Sea Fisheries Research Institute, 106 Nanjing Road, Qingdao, Shandong 266071, P. R. China Location/Qualifiers
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       /organism="Fenneropenaeus chinensis"
/mol_type="genomic DNA"
/db_xref="taxon:139456"
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                                                                             /specific_host="Agaricus
/db_xref="taxon:76883"
                                                                                                                                                                                                                 Length:
                                                                                                              /tissue_type="mycelium"
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               Gaps:
                                             /mol type="genomic DNA"
/isolate="Z15001"

    .98
    /note="microsatellite"

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                 1. .93
/organism="Hypomyces
Location/Qualifiers
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1 (bases 1 to 98)
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72.00
75.00%
46.43%
1.15%
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76.92%
50.00%
1.16%
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/rpt_type=tandem
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53.85%
43.59%
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                                                                                                                                                   PLN 11-DEC-2003
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Arabidopsis thaliana
Bukaryota, Viridiplantaes, Streptophyta; Embryophyta; Tracheophyta;
Spermatophyta; Magnoliophyta; eudicotyledons; core eudicots;
rosids; eurosids II; Brassicales; Brassicaceae; Arabidopsis.
                                                                                                                                                                                                                                     Arabidopsis thaliana
Bukaryota, Viridiplantae, Streptophyta, Embryophyta, Tracheophyta,
Spermatophyta, Magnoliophyta, eudicotyledons, core eudicots,
rosids, eurosids II, Brassicales, Brassicaceae, Arabidopsis.
             422
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                                                                                                                                                                                                                                                                                                                                                                                                                       University of Texas-Austin, 2500
                                                                                                                                                                                                                                                                                           1 (bases 1 to 78)
Symonds, V.V. and Lloyd, A.M.
An Analysis of Microsatellite Loci in Arabidopsis thaliana.
Mutational dynamics and application
Genetics 165 (3), 1475-1488 (2003)
                                                                                                                                      Arabidopsis thaliana Per-2 microsatellite nga8 sequence. AY293995.
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113
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/mol_type="genomic DNA"
/db_xref="taxon:3702"
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/note="microsatellite nga8"
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Symonds, V.V. and Lloyd, A.M.
Direct Submission
Submitted (OB-MAX-2003) MCDB, Univ
Speedway, Austin, TX 78712, USA
Location/Qualifiers
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                                                                    GluGluGluArgArgLysGluIle 430
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AY295846
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Spermatophyta, Magnoliophyta, eudicotyledons, core eudicots,
rosids, eurosids II, Brassicales, Brassicaceae, Arabidopsis.
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Symonds, V.V. and Lloyd, A.M.
An Analysis of Microsatellite Loci in Arabidopsis thaliana.
Mutational dynamics and application
Genetics 165 (13), 1475-1488 (2003)
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             (bases 1 to 77)
Symonds, V.V. and Lloyd, A.W.
An Analysis of Microsatellite Loci in Arabidopsis thaliana.
Mutational dynamics and application
Genetics 165 (3), 1475-1488 (2003)
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 Arabidopsis thaliana Ob-3 microsatellite nga8 sequence. AY293994
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/organism="Arabidopsis thaliana"
/mol type="genomic DNA"
/db_xref="taxon:3702"
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Mismatches:
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    /note="microsatellite nga8"

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Matches:
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Arabidopsis thaliana
                                                                                                                           Symonds, V.V. and Lloyd, A.M.
Symonds, V.V. and Lloyd, A.M.
Direct Submission
Submitted (11-MAY-2003) MCDB, Univ
Speedway, Austin, TX 78712, USA
Location/Qualifiers
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Symonds, V.V. and Lloyd, A.M.
Direct Submission
Submitted (08-MAY-2003) MCDB, Univ
Speedway, Austin, TX 78712, USA
Location/Qualifiers
                                                                                                                                                                                                                                                                                    /organism="Arabidopsis |
/mol_type="genomic DNA"
/db_xref="taxon:3702"
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	Length:	Matches:	Conservative:	Mismatches:	Indels:	Gaps:
	8.85e+04	67.50	51.22%	39.02%	1.08%	8
Alignment Scores:	Pred. No.:	Score:	Percent Similarity:	Best Local Similarity:	Query Match:	DB:

US-09-674-237B-3 (1-1213) x AY293994 (1-77)

390 GlnGluArgiysGluArgGluArgGlnGluGlnGluAlaLysArgGlnLeuGluLeuGlu 409	\GAGAGAGA 27
390 GlnGluArgLysGluArgGlu	AGAGAGA
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Search completed: April 29, 2005, 10:38:23 Job time : 12126 secs

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                                                                                                                                                                                                                                                                                  5' EST; expressed sequence tag; secreted protein; cDNA isolation; nerapy; chromosome mapping; ss.
diagnostic, forensic, gene therapy and chromosome mapping procedures
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            New nucleic acid that is a 5' expressed sequence tag (5' EST) for obtaining cDNAs and genomic DNAs that correspond to 5'ESTs and fo
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 Claim 1; SEQ ID NO 18169; 71pp + Sequence Listing; English.
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                                                                                                                                                                                                                                                  Human secreted protein 5' EST, SEQ ID NO: 18169.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       Giordano J;
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                                   ArgGluAlaAlaLysArgGlu 439
                                                                                                                                                                                                                                                                                                   gene therapy; chromosome mapping;
                                                             AGAGAAGAAGAAGAGAAA 8
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        expression and secretion vectors
                                                                                                                                         AAC14094 standard; cDNA; 87 BP.
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ID AAC1
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392 ArgiysGluArgGluArgGlnGluGluAlaiysArgGlnLeuGluLeuGluLysGln 411

Length:
Matches:
Conservative:
Mismatches:
Indels:

6.74e+04 65.50

52.63% 42.11% 1.04%

Percent Similarity: Best Local Similarity:

Score:

Query Match DB:

Gaps:

US-09-674-237B-3 (1-1213) x AAC14094 (1-87)

87 AGAAAAGAGAGAAAAAAAAGGAAAGAAAGAAAAA----

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412 LeuGluLysGlnArgGluLeuGluArgGlnArgGluGluArgArgLysGlu 429

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The invention relates to an isolated SH3 domain (POSH)-like signalling protein 1 (POSHL 1) polypeptide (I), comprising a sequence of 730 amino acids (SI, ABBB3999), a sequence having 65% sequence identity to (SI), (SI) having 95% deviations, especially conservative substitutions or a fragment of the sequences comprising at least 8 contiguous amino acids. Human POSHL 1 is a proto-oncogene/oncogene product that functions as an adaptor protein that interacts with Rho family Small GTPasses as well as downstream components of the signal transduction pathway. (I) is useful for identifying a specific binding partner. (I) and nucleic acids (II) caused by altered expression of human POSHL1 including diagnosing and treating cancer, they useful in the development of vaccines and (II) is useful in gene therapy. (II) is useful for constructing microarrays which are useful for measuring and for surveying gene expression and creating transgenic non-human animals capable of producing the proteins. The present sequence is that of a single exon probe useful in examples of the printine, but is brand or surveying spart of the printed to be a producing the proteins of the printed to be a produced the protein or but is brand or surveying spart of the printed to be a produced to be a produced the present sequence did not form part of the printed to be a produced to a
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          Novel human SH3 domain (POSH)-like signaling protein 1 polypeptide, POSHL -1, useful for treating disorders associated with decreased expression or activity of human POSHL1.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             specification, but is based on sequence information supplied to Derwent
Human, POSHL 1, SH3 domain, POSH-like signalling protein 1, oncogene,
Rho GTPase; signal transduction, gene expression, cancer, vaccine,
gene therapy, transgenic; probe, ss.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           Example 2; SEQ ID NO 11; 60pp + Sequence Listing; English.
                                                                                                                                                                                                                                                                                                                                                                        30-JAN-2001; 2001WO-US000664.
30-JAN-2001; 2001WO-US000665.
30-JAN-2001; 2001WO-US000666.
30-JAN-2001; 2001WO-US000667.
30-JAN-2001; 2001WO-US000668.
30-JAN-2001; 2001WO-US000669.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           European Patent Office
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               2001US-00864761
2001US-0328205P
                                                                                                                                                                                                                                                                                       28-JAN-2002; 2002EP-00001165
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    WPI; 2002-684061/74
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      (AEOM-) AEOMICA INC
                                                                                                                                                                      EP1239051-A2
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               23-MAY-2001;
10-OCT-2001;
                                                                                                                    Homo sapiens
                                                                                                                                                                                                                                                                                                                                                   30-JAN-2001;
                                                                                                                                                                                                                                     11-SEP-2002.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              Shannon M;
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Seguence 96 BP; 28 A; 16 C; 28 G; 24 T; 0 U; 0 Other;

	w	~				
	96	H	8	8	Н	Н
	Length:	Matches:	Conservative:	Mismatches:	Indels:	Gaps:
	5.94e+04	67.50	70.00%	43.338	1.08%	9
Alignment Scores:	Pred. No.:	Score:	Percent Similarity:	Best Local Similarity:	Query Match:	DB:

US-09-674-237B-3 (1-1213) x ABV89298 (1-96)

```
1020 AspValile -- ValValThrLysLysAspGlyAspTrpTrpThrGlyThrValGlyAsp 1038
                                                                                     63
                                          4 GATATCATCACTGTGATCAGCGAGGGGAGAACTGGGGGGAAGGGAAGTTAGGAGT

4 GATATCATCACTGTGATCAGCGAGGGGAGAACTGGGCAAAGTTAGGAGAT
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LysSerGlyValPheProSerAsnTyrVal 1048 1039

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Isolated or purified higher order aggregate comprising several chimeric molecules having self-coalescing element associated or fused with molecule, useful in chemical, therapeutic and prophylactic applications.
                                                                                                                                               granulocyte-macrophage colony-stimulating factor; GM-CSF; haematopoietic condition; myelosuppressive disorder; AIDS; infectious disease; autoimmune diseases; allergy; viral infection; parasitic infection; cancer; melanoma; leukaemia; lymphoma; cytostatic; anti-HIV; immunosuppressive; antiallergic; antibacterial; virucide; antiparasitic; gene; ds.
93
                                                                                                                                                                                                                                                                                                                                                                                                                                                                         Claim 11; SEQ ID NO 113; 219pp; English.
64 AAAGTAGGCATCTTCCCTATCTTGTTA
                                                                                                                DNA #23.
                                            BP.
                                                                                                                Self-coalescing element (SCE)
                                                                                                                                                                                                                                                                                                   30-MAY-2003; 2003WO-AU000667.
                                                                                                                                                                                                                                                                                                                        31-MAY-2002; 2002US-0384878P.
                                            ADJ36166 standard; DNA; 98
                                                                                        22-APR-2004 (first entry)
                                                                                                                                       Self-coalescing element;
                                                                                                                                                                                                                                 Neisseria meningitidis.
                                                                                                                                                                                                                                                                                                                                               (SCEG-) SCEGEN PTY LID.
                                                                                                                                                                                                                                                                                                                                                                                          WPI; 2004-035460/03.
P-PSDB; ADJ36087.
                                                                                                                                                                                                                                                      WO2003102187-A1.
                                                                                                                                                                                                                                                                                                                                                                      Koentgen F;
                                                                   ADJ36166;
                     RESULT 14
ADJ36166/c
```

comprising several chimeric molecules, where each chimeric molecule has a self-coalescing element (SCE) which is fued, linked or associated with a molecule of interest, and where each SCE is capable of causing individual chimeric molecules to coalesce with other chimeric molecules into higher order aggregates under conditions favourable to aggregation. The aggregate is useful for treating or preventing a disease or condition in patient and has a range of applications including therapeutic, prophylactic and chemical processes. The aggregate comprises a therapeutic polypeptide such as granulocyte-macrophage colony-stimulating factor (GM-CSF), useful for treating haematopoietic conditions such as myelosuppressive disorders e.g. AIDS, infectious diseases, autoimmune diseases, allergies, viral, bacterial and parasitic infections and cancers such as melanoma, leukaemia and lymphoma. This sequence represents DNA encoding an SCE peptide of the invention. The invention relates to an isolated or purified higher order aggregate

Sequence 98 BP; 7 A; 38 C; 6 G; 47 T; 0 U; 0 Other;

```
222716
     Length:
Matches:
Conservative:
Mismatches:
Indels:
Gaps:
    7.23e+04
66.00
85.19%
59.26%
1.05%
                              Best Local Similarity:
                     Percent Similarity:
Alignment Scores:
                                   Query Match:
DB:
        Pred. No.:
```

US-09-674-237B-3 (1-1213) x ADJ36166 (1-98)

413 GluLysGlnArgGluLeuGluArgGlnArgGluGluGluArgArgLysGluIleGluArg 432

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comprising a nucleic acid of the invention. The cotton ESTs are useful as molecular tags to isolate genes, to map and to determine gene to isolate genes, to map genes, to determine gene function and to determining whether genes are members of a particular gene family. The nucleic acid molecules may be used for isolating a variety of agronomically significant genes are associated with plant growth, quality, yield, and could also serve as links in metabolic and catabolic pathways. The nucleic acid molecules are also useful for identifying genes important in initiating and maintaining seed germination or that may be used to militate stresses encountered during seed germination. The ESTs additionally enable the acquisition of promoters and cis-regulatory elements which will be useful to express agronomically significant genes in these tissues and/or other tissues, and also permits the acquisition of molecular markers useful in breeding schemes, genetic and molecular mapping, and in cloning of agronomically significant genes in these tissues and/or other tissues, and also permits the acquisition of molecules are further useful for detecting the presence or quantity of a protein or mRNA and for detecting the presence or quantity of a protein or mRNA and for detecting the presence as specifically claimed EST isolated from a cotton variety Nucotton338 gynoecium tissue cDNA library (LIB3829). The sequence cata for this patent did not form part of the printing the printing patent did not form part of the printing the printing patent did not form part of the printing the printing patent did not form part of the printing the printing patent did not form part of the printing the printing patent did not form part of the printing the p
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  specification, but was obtained in electronic format directly from the US patent office at segdata.uspto.gov/sequence.html?DocID=US20040123340
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            specification, but was obtained in electronic
```

Sequence 73 BP; 0 A; 37 C; 0 G; 36 T; 0 U; 0 Other;

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133
                    Conservative:
Mismatches:
Indels:
      Length:
Matches:
                                          Gaps:
      3.3e + 04
            70.00
79.17%
54.17%
1.12%
13
                            Similarity:
                    Percent Similarity:
Alignment Scores:
                                  Query Match:
DB:
                            Best Local
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409 GluLysGlnLysGlnArgGluLeuGluArgGlnArgGluGluGluArgArgLys 428 요 δ

429 GluileGluarg 432

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ACN61067; RESULT 12
ACN61067/c
1D ACN61
XX
AC ACN61
XX
XX
DT 02-DE
XX
XX
Cotto
XX
Cot

02-DEC-2004 (first entry)

Gossypium hirsutum.

US2004123340-A1.

24-JUN-2004.

14-DEC-2000; 2000US-0255619P

(DEIK/) DEIXMAN J. (FENG/) FENG P C C. (FINC/) FINCHER K L. (ZIEG/) ZIEGLER T E.

US-09-674-237B-3 (1-1213) x ACN59545 (1-73)

13 GAGAGAGAGA 2

ACN61067 standard; cDNA; 76 BP.

Cotton gynoecium tissue EST Clone ID: LIB3829-031-Q6-N6-C11, SEQ:15848.

Cotton; plant; EST; expressed sequence tag; transgenic plant; gynoecium; variety Nucotton33B; library LIB3829; molecular tag; molecular marker; genetic mapping; molecular mapping; seed germination; plant growth; plant quality; plant yield; plant breeding; tissue printing; ss.

12-DEC-2001; 2001US-00021323

Ziegler TE; Fincher KL, Feng PCC, Deikman J,

WPI; 2004-479808/45.

New isolated nucleic acid molecule that encodes a plant protein or its fragment, useful for isolating a variety of agronomically significant genes associated with plant growth, quality or yield, and as molecular tags to map genes.

Claim 1; SEQ ID NO 15848; 34pp; English.

molecular tage to isolate genetic regions, to isolate genes, to map genes, to determine gene function and to determining whether genes are members of a particular gene family. The nucleic acid molecules may be used for isolating a variety of againty. The nucleic acid molecules may be used for isolating a variety of againty, yield, and could also serve as links in metabolic and catabolic pathways. The nucleic acid molecules are also useful for identifying genes important in initiating and maintaining seed germination or that may be used to mitigate stresses encountered during seed germination. The BSTs additionally enable the acquisition of promoters and cis-regulatory elements which will be useful to express agronomically significant genes in these tissues and/or other tissues, and also permits the acquisition of molecular mapping, and in cloning of agronomically significant genes. The nucleic acid molecules are further useful for significant genes. The nucleic acid molecules are further useful for significant genes. The nucleic acid molecules are further useful for significant genes. The nucleic acid molecules are further useful for significant genes or quantity of a protein or mRNA and for detecting the presence or quantity of a protein by tissue printing. The present sequence represents a specifically claimed EST isolated from a cotton variety Nucotroning part of a protein by tissue printing sequence data for this patent did not form part of the printed sequence data for this patent did not form part of formed protein the useful for specification, but was obtained in electronic former form The invention relates to 17880 cotton expressed sequence tags (ESTS; ACN45220-ACN63099). The ESTS were isolated from cDNA libraries generated from primed or non-primed seeds from variety DESOB, mature seeds from variety Coker 312 Boswell 96 Field, and androecium tissue, gynoccium tissue, developing fibres, carpel walls and septa from variety Nucotton33B. The invention also relates to substantially purified proteins or their fragments encoded by nucleic acid molecules of the invention, and to transformed plants having a nucleic acid construct comprising a nucleic acid of the invention. The cotton ESTS are useful as specification, but was obtained in electronic format directly from th patent office at seqdata.uspto.gov/sequence.html?DocID=US20040123340

%X3XCCCCCCCCCCCCCCCCCCCCCCCCCCCX

Sequence 76 BP; 0 A; 38 C; 0 G; 38 T; 0 U; 0 Other;

76 113 0 0 Conservative: Mismatches: Indels: Length: Matches: 3.45e+04 70.00 79.17% 54.17% 1.12% Best Local Similarity: Percent Similarity: Alignment Scores: Query Match: Pred. No.:

US-09-674-237B-3 (1-1213) x ACN61067 (1-76)

409 GluLysGlnLeuGluLysGlnArgGluLeuGluArgGlnArgGluGluGluArgArgLys 428 쉽

429 GluileGluArg 432 15 GAGAGAGAGAGA RESULT 13 ABV89298 ઠે 셤

BP

ABV89298 standard; DNA; 96

23-DEC-2002 (first entry) ABV89298;

2×2×4×8×

Human POSHL1 single exon probe SEQ ID NO 11.

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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   preventing diagnosing disorders.
                                              \mathbf{n}
                                                                                                                                                                                                                                                                              407 GluLeuGluLysGlnLeuGluLysGlnArgGluLeuGluArgGlnArgGluGluGluArg 426
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           The invention relates to human polynucleotides (AAI79941-AAI93841) and the encoded proteins (AA000010-AA013910) that exhibit activity elating to cytokine, cell proliferation or cell differentiation or which may induce production of other cytokines in other cell populations. The polymetides and polypeptides are useful in gene therapy, vaccines or peptide therapy. The polypeptides have various cytokine-like activities, e.g. stem cell growth factor activity, immunomodulatory activity and activity, tissue growth factor activity, immunomodulatory activity and activin/inhibin activity and may be useful in the diagnosis and/or
                                                                                                                                                                                                                                                                                              Human; cytokine; cell proliferation; cell differentiation; gene therapy;
cotton variety Nucotton33B gynoecium tissue cDNA library (LIB3829). The sequence data for this parent did not form part of the printed specification, but was obtained in electronic format directly from the U patent office at segdata.uspto.gov/sequence.html?bocID=US20040123340
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       vaccine; peptide therapy; stem cell growth factor; haematopolesis;
tissue growth factor; immunomodulatory; cancer; leukaemia;
nervous system disorders; arthritis; inflammation; ss.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 Claim 1; SEQ ID NO 4801; 1399pp + Sequence Listing; English.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 ated nucleic acids and polypeptides, useful for treating e.g. leukemia, inflammation and immune
                                                                                                                                        81
6
6
0
0
0
                                                                                         0 A; 41 C; 0 G; 40 T; 0 U; 0 Other;
                                                                                                                                                                   Conservative:
Mismatches:
Indels:
                                                                                                                                        Length:
Matches:
                                                                                                                                                                                                                   Gaps:
                                                                                                                                                                                                                                                (1-81)
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               Human polynucleotide SEQ ID NO 4801
                                                                                                                                                                                                                                                US-09-674-237B-3 (1-1213) x ACN59315
                                                                                                                                                                                                                                                                                                                                             432
                                                                                                                                                                                                                                                                                                                                                                                                                                     BP
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               26-FEB-2001; 2001WO-US004927
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              28-FEB-2000; 2000US-00515126
18-MAY-2000; 2000US-00577409
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        Tang YT, Liu C, Drmanac RT
                                                                                                                                     2.61e+04
73.00
76.92%
53.85%
1.16%
                                                                                                                                                                                                                                                                                                                                          427 ArgLysGlulleGluArg
                                                                                                                                                                                                                                                                                                                                                             21 GAGAGAGAGAGAGAGA
                                                                                                                                                                                                                                                                                                                                                                                                                                    AAI84741 standard; cDNA; 98
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                (first entry)
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        WPI; 2001-514838/56.
                                                                                                                                                                     Percent Similarity:
Best Local Similarity:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            (HYSE-) HYSEQ INC.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      P-PSDB; AAO04810
                                                                                         Sequence 81 BP;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      WO200164835-A2
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       Homo sapiens.
                                                                                                                        Alignment Scores:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               06-NOV-2001
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  07-SEP-2001
                                                                                                                                                                                                                                                                                                                                                                                                                                                                    AAI84741;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      Isolated
                                                                                                                                                                                                     Query Match:
DB:
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                                                                                                                                                                                                                                                                                                                                                                                                       RESULT 10
                                                                                                                                                                                                                                                                                                                                                                                                                    셤
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413 GlubysGlnArgGlubeuGluArgGlnArgGluGluGluArgArgLysGluIleGluArg 432
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           The invention relates to 17880 cotton expressed sequence tags (ESTs; ACM 92209). The ESTs were isolated from CDNA libraries generated from primed or non-primed seeds from variety DP508, mature seeds from variety Coker 312 Boswell 96 Field, and androecium tissue, gynoecium tissue, developing fibres, carpel walls and septer from variety Nucotton318. The invention also relates to substantially purified proteins or their fragments encoded by nucleic acid molecules of the
                                                                                                                                                                                                                                                                                             Cotton; plant; EST; expressed sequence tag; transgenic plant; gynoecium; variety Nucotton33B; library LIB3829; molecular tag; molecular marker; genetic mapping; molecular mapping; seed germination; plant growth; plant quality; plant yield; plant breeding; tissue printing; ss.
treatment of cancer, leukaemia, nervous system disorders, arthritis and inflammation. Note: The sequence data for this patent did not form part of the printed specification, but was obtained in electronic format directly from WIPO at ftp.wipo.int/pub/published_pct_sequences
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            New isolated nucleic acid molecule that encodes a plant protein or its fragment, useful for isolating a variety of agronomically significant genes associated with plant growth, quality or yield, and as molecular
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     Cotton gynoecium tissue EST Clone ID: LIB3829-032-Q6-N6-C5, SEQ:14326
                                                                             BP; 37 A; 11 C; 50 G; 0 T; 0 U; 0 Other;
                                                                                                                              984 99 0
                                                                                                                            Length:
Matches:
Conservative:
Mismatches:
Indels:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 TE;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   Ziegler
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               Claim 1; SEQ ID NO 14326; 34pp; English.
                                                                                                                                                                                                             Gaps:
                                                                                                                                                                                                                                            US-09-674-237B-3 (1-1213) x AAI84741 (1-98)
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   Fincher KL,
                                                                                                                                                                                                                                                                                                                                                                                                                                          BP
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     12-DEC-2001; 2001US-00021323.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  14-DEC-2000; 2000US-0255619P.
                                                                                                                                                                                                                                                                                                                                            433 ArgGluAlaAlaLys 437
                                                                                                                                                                                                                                                                                                                                                                          84
                                                                                                                         3.2e+04
73.00
76.00%
56.00%
1.16%
                                                                                                                                                                                                                                                                                                                                                                                                                                         ACNS9545 standard; cDNA; 73
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       (first entry)
                                                                                                                                                                                                                                                                                                                                                                          70 GAGAGCGCGCGCGG
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   Deikman J, Feng PCC,
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              (DEIK/) DEIKMAN J.
(FENG/) FENG P C C.
(FINC/) FINCHER K L.
(ZIEG/) ZIEGLER T E.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 WPI; 2004-479808/45.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     Gossypium hirsutum
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                tags to map genes.
                                                                                                                                                                               Best Local Similarity:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     US2004123340-A1
                                                                                                                                                              Percent Similarity:
                                                                                                               Alignment Scores:
                                                                               Sequence 98
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         02-DEC-2004
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     24-JUN-2004
                                                                                                                                                                                                                                                                                                                                                                                                                                                                          ACN59545;
                                                                                                                                                                                              Query Match:
                                                                                                                                Pred. No.:
                                                                                                                                                                                                                                                                                                                                                                                                            RESULT 11
                                                                                                                                                                                                                                                                                                                                                                                                                           ACN59545/
                                                                                                                                               Score:
 8888888
                                                                                                                                                                                                                                                                                                                                                                         임
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New nucleic acid construct capable of high efficiency delivery of polynucleotides into DNA containing organelles, e.g. nucleus, comprises a first, a second, and optionally, a third polynucleotide segment.
                                                                                                                  nucleic acid construct; vaccine; nucleic acid recognition sequence;
                                                                                                  Peptide nucleic acid (PNA) recognition sequence SEQ ID NO:2.
433 ArgGluAlaAlaLysArgGluLeuGluArgGlnArgGln 445
        Example 1; Page 46; 46pp; English.
                                                 ВЪ
                                                                                                                                                                                                                                        (YEDA ) YEDA RES & DEV CO LTD
                                                                                                                                                                                                       17-SEP-2002; 2002WO-IL000772.
                                                                                                                                                                                                                        17-SEP-2001; 2001US-0322449P.
                                                                                                                  Kappa B motif; pGL3 vector;
DNA transformation; peptide
                                                 ACC69626 standard; DNA; 88
                                                                                  (first entry)
                                                                                                                                                                                                                                                                          WPI; 2003-371818/35.
                                                                                                                                    vaccination; ss.
                                                                                                                                                                     WO2003025195-A2
                                                                                  18-JUL-2003
                                                                                                                                                                                      27-MAR-2003
                                                                                                                                                     Synthetic.
                                                                                                                                                                                                                                                          Reich Z;
                                        ሯ
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The present invention describes a nucleic acid construct. The nucleic acid construct comprises: (a) a first polynucleotide segment including at least one nucleic acid sequence element; and (b) a second polynucleotide segment encoding a polypeptide including a nucleic acid binding domain being capable of specifically binding the above nucleic acid sequence element, and a localisation signal for directing transport of the polypeptide into a DNA containing organelle such that when the nucleic acid construct is introduced into a cell, expression of the polypeptide from the second polynucleotide segment directs transport of the nucleic acid construct into the DNA containing organelle. The nucleic acid construct is useful in high efficiency delivery of polynucleotides into DNA containing organelles such as nucleus, chloroplast or mitochondria, and containing organelles such as nucleus, chloroplast or mitochondria, and approaches designed for therapeutic purposes. The nucleic acid construct may also be used to isolate novel genes encoding nucleic acid sequence. ig proteins. The present sequence represents a peptide nucleic acid recognition sequence, which is used in an example from the present invention binding

Claim 1; SEQ ID NO 14096; 34pp; English.

tags to map genes.

Sequence 88 BP; 1 A; 44 C; 2 G; 41 T; 0 U; 0 Other;

```
888
77
77
14
     Length:
Matches:
Conservative:
Mismatches:
Indels:
                                                Gaps:
      1.79e+04
              77.00
72.73$
51.52$
1.23$
                              Similarity:
                       Percent Similarity:
Alignment Scores:
                                       Query Match:
                                Best Local
```

US-09-674-237B-3 (1-1213) x ACC69626 (1-88)

```
Cotton; plant; EST; expressed sequence tag; transgenic plant; gynoecium; variety Nucotton13B; library LIBS829; molecular tag; molecular marker; genetic mapping; molecular mapping; seed germination; plant growth; plant quality; plant yield; plant breeding; tissue printing; ss.
                                                                                                                                                                                                                                                                                                                                                                                                               New isolated nucleic acid molecule that encodes a plant protein or its fragment, useful for isolating a variety of agronomically significant genes associated with plant growth, quality or yield, and as molecular
                                                                                                                                                    Cotton gynoecium tissue EST Clone ID: LIB3829-029-Q6-N6-D1, SEQ:14096.
                               433 ArgGluAlaAlaLysArgGluLeuGluArgGlnArgGln 445
                                          Ziegler TE;
                                                                                                                                                                                                                                                                                                                                                                          Fincher KL,
                                                                                                                                                                                                                                                                                 12-DEC-2001; 2001US-00021323.
                                                                                                                                                                                                                                                                                                     14-DEC-2000; 2000US-0255619P.
                                                                                        ACNS9315 standard; cDNA; 81
                                                                                                                                (first entry)
                                                                                                                                                                                                                                                                                                                                                                          Deikman J, Feng PCC,
                                                                                                                                                                                                                                                                                                                       (DEIK/) DEIKMAN J.
(FENG/) FENG P C C.
(FINC/) FINCHER K L.
(ZIEG/) ZIEGLER T E.
                                                                                                                                                                                                                                                                                                                                                                                             WPI; 2004-479808/45.
                                                                                                                                                                                                                       Gossypium hirsutum
                                                                                                                                                                                                                                           US2004123340-A1.
                                                                                                                                02-DEC-2004
                                                                                                                                                                                                                                                              24-JUN-2004.
                                                                                                            ACN59315;
                                                                     RESULT 9
                                                                                 ACN59315,
```

The invention relates to 17880 cotton expressed sequence tags (ESTB;
ACM45220-ACN63099). The ESTB were isolated from cDNA libraries generated
CC ACM45220-ACN63099). The ESTB were isolated from cDNA libraries generated
CC from prined seeds from variety DPSOB, mature seeds from
variety Coker 312 Boswell 96 Field, and androecium tissue, gynoecium
curiety Coker 312 Boswell 96 Field, and androecium tissue, gynoecium
curiety Coker 312 Boswell 96 Field, and septa from variety
CC Nucotton3B. The invention also relates to substantially purified
cromprising a nucleic acid of the invention. The cotton ESTB are useful as
molecular tags to isolate genetic regions, to isolate genes, to map
C genes, to determine gene function and to determining whether genes
C genes, to determine gene family. The nucleic acid molecules may be
used for isolating a variety of agronomically significant genes
c used for isolating a variety of agronomically significant genes
c associated with plant growth, quality, yield, and could also serve as
links in metabolic and catabolic pathways. The nucleic acid molecules are
also useful for identifying genes important in initiating and maintaining
seed germination or that may be used to miligate stresses encountered
during seed germination. The ESTB additionally enable the acquisition of
compress and catabolic acid molecular markers useful in breeding
conformically significant genes in these tissues and/or other tissues,
adronomically significant genes in these tissues are further useful for
schemes, genetic and molecular mapping, and in cloning of agronomically
significant genes or quantity of a protein or mRNA and for
detecting the expression level or pattern of a protein or mRNA and for
detecting the presence or quantity of a protein or mRNA and for

Gossypium hirsutum.

New isolated nucleic acid molecule that encodes a plant protein or its fragment, useful for isolating a variety of agronomically significant genes associated with plant growth, quality or yield, and as molecular tags to map genes.

Claim 1; SEQ ID NO 15706; 34pp; English

The invention relates to 17880 cotton expressed sequence tags (ESTs; ACN45220-ACN63099). The ESTs were isolated from cDNA libraries generated from parimed over an order to the ESTs were isolated from cDNA libraries generated from variety Coker 312 Boswell 96 Field, and androecium tissue, gynoecium tissue, developing fibres, carpel walls and septe from variety isolated. The invention also relates to substantially purified proteins or their fragments encoded by nucleic acid molecules of the invention, and to transformed plants having a nucleic acid construct comprising a nucleic acid of the invention. The cotton ESTs are useful as molecular tags to isolate genetic regions, to isolate genes to mapped genes, to determine gene function and to determining whether genes are useful for isolating a variety of agronomically significant genes are useful for isolating a variety of agronomically significant genes as associated with plant growth, quality, yield, and could also serve as links in metabolic and catabolic pathways. The nucleic acid molecules are also useful for identifying genes important in initiating and maintaining seed germination or that may be used to mitigate stresses encountered during seed germination. The ESTs additionally enable the acquisition of promoters and cis-regulatory elements which will be useful to express and also permits the acquisition of molecular markers useful in breeding schemes, genetic and molecular mapping, and in cloning of agronomically capened and indicated genetic and molecular mapping, and in cloning of agronomically detecting the expression level or pattern of a protein or man and expression level or pattern of a protein or man and expression level or pattern of a protein or man and expression level or pattern of a protein or man and expression level or pattern of a protein or man and expression level or pattern of a protein or man and expression level or pattern of a protein or man and expression level or pattern of a protein or man and expression level or pattern of a prote specification, but was obtained in electronic format directly from the US patent office at segdata.uspto.gov/sequence.html?DocID=US20040123340 cotton variety Nucotton33B gynoecium tissue cDNA library (LIB3829). The sequence data for this patent did not form part of the printed specification, but was obtained in electronic format directly from the D

Sequence 89 BP; 0 A; 45 C; 0 G; 44 T; 0 U; 0 Other;

Conservative: Mismatches: Length: Matches: Indels: 1.43e+04 79.00 72.73% 51.52% 1.26% Similarity: Percent Similarity: Alignment Scores: Pred. No.: Query Match: Best Local

JS-09-674-237B-3 (1-1213) x ACN60925 (1-89)

413 GluLysGlnArgGluLeuGluArgGlnArgGluGluGluArgArgLysGluIleGluArg 432 셤

433 ArgGluAlaAlaLy8ArgGluLeuGluArgGlnArgGln 445

ò

ACN59554, RESULT 7

ACN59554 standard; cDNA; 89 BP.

(first entry) 02-DEC-2004

ACN59554;

Cotton gynoecium tissue EST Clone ID: LIB3829-032-Q6-N6-F1, SEQ:14335.

Cotton; plant; EST; expressed sequence tag; transgenic plant; gynoecium; variety Nucotton318; library LIBS29; molecular tag; molecular marker; genetic mapping; molecular mapping; seed germination; plant growth; plant quality; plant yield; plant breeding; tissue printing; ss. 

Ziegler TE; Fincher KL, .2-DEC-2001; 2001US-00021323. 14-DEC-2000; 2000US-0255619P Deikman J, Feng PCC, FINCHER K L. ZIEGLER T E. DEIKMAN J. FENG P C C. US2004123340-A1. 24-JUN-2004 (FINC/) DEIK/) FENG/) 

WPI; 2004-479808/45.

New isolated nucleic acid molecule that encodes a plant protein or its fragment, useful for isolating a variety of agronomically significant genes associated with plant growth, quality or yield, and as molecular tags to map genes.

Claim 1; SEQ ID NO 14335; 34pp; English.

The invention relates to 17880 cotton expressed sequence tags (ESTB;
ACN45220-ACN63099). The ESTB were isolated from cDNA libraries generated
ACN45220-ACN63099). The ESTB were isolated from cDNA libraries generated
CC from primed seeds from variety DPSOB, mature seeds from
variety Coker 312 Boswell 96 Field, and and rectum tissue, gynoecium
tissue, developing fibres, carpel walls and septa from variety
CC Mucotton33B. The invention also relates to substantially purified
proteins or their fragments encoded by nucleic acid molecules of the
invention, and to transformed plants having a nucleic acid construct
comprising a nucleic acid of the invention. The cotton ESTB are useful as
molecular tags to isolate genetic regions, to isolate genes, to determine gene function and to determining whether genes are
cc members of a particular gene family. The nucleic acid molecules may be
genes, to determine gene family. The nucleic acid molecules may be
used for isolating a variety of agronomically significant genes
cs associated with plant growth, quality, yield, and could also serve as
links in metabolic and catabolic pathways. The nucleic acid molecules are
also useful for identifying genes important in initiating and maintaining
seed germination or that may be used to mitigate stresses encountered
during seed germination. The ESTB additionally enable the acquisition of
promoters and cis-regulatory elements which will be useful to express
cd agronomically significant genes in these tissues and/or other tissues,
and also permits the acquisition of molecular markers useful in breeding
schemes, genetic and molecular mapping, and in cloning of agronomically
cdetecting the expression level or pattern of a protein or mRNA and for
detecting the presence or quantity of a protein or mRNA and for
checking the wardersole as specifically claimed Bones.
COTTON variety and molecular results and protein or mRNA and correction variety. the US cotton variety Nucottonil gynoecium tissue cDNA library (LIB3829). The sequence data for this patent did not form part of the printed specification, but was obtained in electronic format directly from the U patent office at segdata.uspto.gov/sequence.html?DocID=US20040123340

Sequence 89 BP; 0 A; 44 C; 0 G; 45 T; 0 U; 0 Other;

89 7 7 7 17 4 17 7 Conservative: Mismatches: Matches: Length: Indels: 1.43e + 0479.00 72.73% 51.52% 1.26% Similarity: Percent Similarity: Best Local Similarit Alignment Scores: Pred. No.: Query Match Score:

US-09-674-237B-3 (1-1213) x ACN59554 (1-89)

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413 GluLysGlnArgGluLeuGluArgGlnArgGluGluGluArgArgLysGluIleGluArg 432 

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96
117
00
00
00
48 T; 0 U; 1 Other;
                        Length:
Matches:
Conservative:
Mismatches:
Indels:
                                                                     Gaps:
A; 47 C; 0 G;
                                 84.00
68.75%
53.12%
1.34%
0
                                         Percent Similarity:
Best Local Similarity:
Sequence 96 BP;
                  Alignment Scores:
                                                           Match
                          ..
No.:
                                                           Query 1
DB:
```

(1-96)US-09-674-237B-3 (1-1213) x ACN59485

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413 GluLysGlnArgGluLeuGluArgGlnArgGluGluGluArgArgLysGluIleGluArg 432
                                             433 ArgGluAlaAlaLysArgGluLeuGluArgGlnArg 444
                                                                                                     ઠે
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36 GAGAGAGAGAGAGAGAGAGAGAGAGAGANAGAGA 1

ACN46027 standard; cDNA; 88 RESULT 5 ACN46027/

ACN46027;

(first entry)

02-DEC-2004

Cotton primed seed EST Clone ID: LIB3825-013-Q1-N6-D1, SEQ:808,

Cotton; plant; EST; expressed sequence tag; transgenic plant; seed; variety DPSOB; library LIB3825; molecular tag; molecular marker; genetic mapping; molecular mapping; seed germination; plant growth; plant quality; plant yield; plant breeding; tissue printing; ss.

Gossypium hirsutum

US2004123340-A1.

24-JUN-2004.

L2-DEC-2001; 2001US-00021323

14-DEC-2000; 2000US-0255619P.

DEIK/)

DEIKMAN J. FENG P C C. FINCHER K L. ZIEGLER T E. (FENG/) (FINC/) (ZIEG/) Ziegler TE; Fincher KL, Deikman J, Feng PCC,

WPI; 2004-479808/45.

New isolated nucleic acid molecule that encodes a plant protein or its fragment, useful for isolating a variety of agronomically significant genes associated with plant growth, quality or yield, and as molecular tags to map genes.

Claim 1; SEQ ID NO 808; 34pp; English.

The invention relates to 17880 cotton expressed sequence tags (ESTs; ACN45220-ACN63099). The ESTs were isolated from cDNA libraries generated from primed or non-primed seeds from variety Debols, mature seeds from variety Coker 312 Boswell 96 Field, and androecium tissue, gynoecium tissue, developing fibres, carpel walls and septa from variety Nucotton338. The invention also relates to substantially purified proteins or their fragments encoded by nucleic acid molecules of the invention, and to transformed plants having a nucleic acid construct comprising a nucleic acid of the invention. The cotton ESTs are useful as molecular tags to isolate genetic regions, to isolate genes, to map genes, to determine gene function and to determining whether genes are members of a particular gene family. The nucleic acid molecules may be

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used for isolating a variety of agronomically significant genes
associated with plant growth, quality, yield, and could also serve as
links in metabolic and catabolic pathways. The nucleic acid molecules
also useful for identifying genes important in initiating and maintaining
seed germination or that may be used to mitigate stresses encountered
during seed germination. The BSTs additionally enable the acquisition of
promoters and cis-regulatory elements which will be useful to express
agronomically significant genes in these tissues and/or other tissues,
and also permits the acquisition of molecular markers useful in breeding
schemes, genetic and molecular mapping, and in cloning of agronomically
significant genes. The nucleic acid molecules are further useful for
detecting the expression level or pattern of a protein or mRNA and for
detecting the presence or quantity of a protein by tissue printing. The
present sequence represents a specifically claimed BST isolated from a
cotton variety bps08 primed seed cDNA library (LIB3825). The sequence
data for this patent did not form part of the printed specification, but
was obtained in electronic format directly from the US patent office at
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          seqdata.uspto.gov/sequence.html?DocID=US20040123340
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G; 44 T; 0 U; 0 Other; Sequence 88 BP; 0 A; 44 C; 0

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88
117
7
5
                      Conservative:
Mismatches:
Indels:
       Length:
Matches:
                                              Gaps:
1.42e+04
79.00
72.73$
51.52$
1.26$
                                Best Local Similarity:
                       Percent Similarity:
Alignment Scores:
                                       Query Match:
DB:
         ..
0
..
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(1-88)US-09-674-237B-3 (1-1213) x ACN46027 413 GluLysGlnArgGluLeuGluArgGlnArgGluGluGluArgArgLysGluIleGluArg 432 

---GAGAGAGAGAGAGAGAGAGAGAG

433 ArgGluAlaAlaLysArgGluLeuGluArgGlnArgGln 445

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ACN60925, RESULT 6

ACN60925 standard; cDNA; 89

ACN60925;

02-DEC-2004 (first entry)

Cotton gynoecium tissue EST Clone ID: LIB3829-029-06-N6-B7, SEQ:15706.

Cotton; plant; EST; expressed sequence tag; transgenic plant; gynoecium; variety Nucotton33B; library LIB3829; molecular tag; molecular marker; genetic mapping; molecular mapping; seed germination; plant growth; plant quality; plant yield; plant breeding; tissue printing; ss.

Gossypium hirsutum

US2004123340-A1.

24-JUN-2004.

12-DEC-2001; 2001US-00021323

14-DEC-2000; 2000US-0255619P (DEIK/) 

DEIKMAN J. FENG P C C. FINCHER K L. ZIEGLER T E. ZIEG/) FINC/) FENG/)

Ziegler TE; Fincher KL, Deikman J, Feng PCC,

WPI; 2004-479808/45

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Deikman J, Feng PCC, Fincher KL,
         12-DEC-2001; 2001US-00021323.
                14-DEC-2000; 2000US-0255619P.
                       (DEIK/) DEIKMAN J.
(FENG/) FENG P C C.
(FINC/) FINCHER K L.
(ZIEG/) ZIEGLER T E.
                                               WPI; 2004-479808/45
                                                                 tags to map genes.
   24-JUN-2004.
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Ziegler TE;

New isolated nucleic acid molecule that encodes a plant protein or its fragment, useful for isolating a variety of agronomically significant genes associated with plant growth, quality or yield, and as molecular

Claim 1; SEQ ID NO 14338; 34pp; English.

The invention relates to 17880 cotton expressed sequence tags (ESTE;
ACNA5220-ACN63099). The ESTS were isolated from cDNA libraries generated
from primed or non-primed seeds from variety DPSOB, mature seeds from
variety Coker 312 Boswell 96 Field, and androecium tissue, gynoecium
tissue, developing fibres, carpel walls and septa from variety
CC tissue, developing fibres, carpel walls and septa from variety
CC Nucotton33B. The invention also relates to substantially purified
proteins or their fragments encoded by nucleic acid molecules of the
invention, and to transformed plants having a nucleic acid construct
CC comprising a nucleic acid of the invention. The cotton ESTS are useful
cc invention, and to transformed plants having a nucleic acid construct
CC comprising a nucleic acid of the invention. The cotton ESTS are useful
cc sused for isolate genetic regions, to isolate genes
cc members of a particular gene family. The nucleic acid molecules may be
CC used for isolating a variety of agronomically significant genes
cc associated with plant growth, quality, yield, and could also serve as
CC links in metabolic and catabolic pathways. The nucleic acid molecules are
calso useful for identifying genes important in initiating and molecules
cc associated with plant growth, quality, yield, and could also serve as
clinks in metabolic and catabolic pathways. The nucleic acid molecules
cc during seed germination. The ESTs additionally enable the acquisition of
ced germination or that may be used to mitigate stresses encountered
cc during seed germination. The ESTs additionally enable the acquisition of
condenses, genetic and molecular mapping, and in cloning of agronomically
significant genes. The nucleic acid molecules may price or genetic tand molecular mapping, and in cloning of agronomically
significant genes. The nucleic acid molecules on the printed
cc detecting the expression level or pattern of a protein or mRNA and for
detecting the expression level or pattern of a protein or mRNA account and sequence atta for specification, but was obtained in electronic format directly from the US patent office at segdata.uspto.gov/sequence.html?DocID=US20040123340

Sequence 99 BP; 0 A; 50 C; 0 G; 49 T; 0 U; 0 Other;

	66	17	7	თ	0	0
	Length:	Matches:	Conservative:	Mismatches:	Indels:	Gaps:
	5.03e+03					13
Alignment Scores:	Pred. No.:	Score:	Percent Similarity:	Best Local Similarity:	Query Match:	DB:

US-09-674-237B-3 (1-1213) x ACN59557 (1-99)

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413 GluLysGlnArgGluLeuGluArgGlnArgGluGluGluArgArgLysGluIleGluArg 432
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133 ArgGluAlaAlaLysArgGluLeuGluArgGlnArgGln 445

Cotton; plant; BST; expressed sequence tag; transgenic plant; gynoecium; variety Nucotton38; library LIB3829; molecular tag; molecular marker; genetic mapping; molecular mapping; seed germination; plant growth; plant quality; plant yield; plant breeding; tissue printing; ss. Cotton gynoecium tissue EST Clone ID: LIB3829-031-Q6-N6-G3, SEQ:14266. BP. ACN59485 standard; cDNA; 96 02-DEC-2004 (first entry) ACN59485; ACN59485/c 

Gossypium hirsutum. US2004123340-A1.

24-JUN-2004.

12-DEC-2001; 2001US-00021323

14-DEC-2000; 2000US-0255619P

DEIKMAN J. FENG P C C. (DEIK/) (FENG/)

FINCHER K L. ZIEGLER T E. (FINC/) Fincher KL, Ziegler TE; Deikman J, Feng PCC,

WPI; 2004-479808/45.

New isolated nucleic acid molecule that encodes a plant protein or its fragment, useful for isolating a variety of agronomically significant genes associated with plant growth, quality or yield, and as molecular tags to map genes.

Claim 1; SEQ ID NO 14266; 34pp; English.

The invention relates to 17880 cotton expressed sequence tags (ESTS;

ACN45220-ACN63099). The ESTS were isolated from cDNA libraries generated
from primed or non-primed seeds from variety DP50B, mature seeds from
variety Coker 312 Boswell 96 Field, and androecium tissue, gynoecium
tissue, developing fibres, carpel walls and septa from variety

Nucotton33B. The invention also relates to substantially purified
comprising a nucleic acid of the invention. The cotton ESTS are useful as
invention, and to transformed plants having a nucleic acid construct
comprising a nucleic acid of the invention. The cotton ESTS are useful as
combecular tags to isolate genetic regions, to isolate genes to members of a particular gene function and to determining whether genes are
comparising a variety of agronomically significant genes are
members of a particular gene family. The nucleic acid molecules may be
compared with plant growth, quality, yield, and could also serve as
links in metabolic and catabolic pathways. The nucleic acid molecules are
also useful for identifying genes important in initiating and maintaining
seed germination or that may be used to mitigate stresses encountered
during seed germination. The ESTs additionally enable the acquisition of
promoters and cis-regulatory elements which will be useful to express
comparison genes; the acquisition of molecular markers useful in breeding
schemes, genetic and molecular mapping, and in cloning of agronomically
significant genes in these tissues are further useful for
detecting the expression level or pattern of a protein or mRNA and for
detecting the presence or quantity of a protein by tissue printing. The
correct or variety whorternally canned in the presence as geoedically clanded a protein or mRNA in practice.

Control to the presence or quantity of a protein by tissue printing. The cotton variety Nucotton33B gynoecium tissue cDNA library (LIB3829). The sequence data for this patent did not form part of the printed specification, but was obtained in electronic format directly from the US patent office at seqdata.uspto.gov/sequence.html?DocID=US20040123340

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number of oligonucleotides derived from an orthologue gene of a different organism or species immobilised on a support body. The oligonucleotide array has two sides comprising a gene derived from two different corganisms, in which one side comprises a human gene. In the oligonucleotide array a base sequence differs in a different position on the support body. Each of the oligonucleotides is a partial sequence of the organism and organisms B. The sequence match degree of the organism species A and the organism species B is less than the organism species A and the organism species B is the level-of. The sequence handless and the organism species B is the level-of. The squares species A and the organism species B is the level-of. The cyanism species A and the organism species B is the level-of. The cyanism species A and the organism species B is the level-of. The organism species A and the organism species B is the level-of. The cyanism species A and the organism species C or more. The found value or the calculated value of the malting-temperature of the variant genes other than the orthologue gene of the cyanism species B is 20 degrees C or more. The oligonucleotide array is useful for measuring expression distribution of the orthologue gene in different organisms. The method is useful for comparing expression change of the orthologue gene in different organisms. The method is useful for medical agent administration and for comparing change of the function of the orthologue gene in different organisms. The oligonucleotide array has the orthologue gene in different organisms. The oligonucleotide array is two or more types of organism simultaneously. The oligonucleotide array is two or more types of organism simultaneously. The oligonucleotide array is in the oligonucleotide array of the invention.
different organism immobilized on support
                                                                                                                               Disclosure; Page 16; 56pp; Japanese.
gene of
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Sequence 80 BP; 19 A; 15 C; 25 G; 21 T; 0 U; 0 Other;

```
000088
      Length:
Matches:
Conservative:
                            Mismatches:
Indels:
      1.84
155.00
100.00%
100.00%
2.47%
                               Best Local Similarity:
                      Percent Similarity:
Alignment Scores:
                                    Query Match:
DB:
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US-09-674-237B-3 (1-1213) x ADP49483 (1-80)

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940 AspMetTrpTrpPheGlyGluValGlnGlyGlnLysGlyTrpPheProLysSerTyrVal 959
                    61
            960 LysLeulleSerGlyPro 965
                    ~
                     g
                                          ò
 8
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AAACTCATTTCAGGGCCC 79

ABN38018 standard; DNA; 60 RESULT 2

BP

ABN38018;

(first entry) 15-JUL-2002 Human spliced transcript detection oligonucleotide SEQ ID NO:10766.

Human, mouse, rat, splice transcript, detection, RNA transcript, splice variant; transcriptome, oligonucleotide library, ss.

Homo sapiens

WO200210449-A2

07-FEB-2002.

20-JUL-2001; 2001WO-IB001903

28-JUL-2000; 2000US-0221607P.

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02-MAY-2001; 2001US-0287724P.
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(COMP-) COMPUGEN INC.

Faigler S; Mintz L, Mintz E, Wasserman A, Shoshan A,

WPI; 2002-257383/30.

New oligonucleotide libraries comprising oligonucleotides which selectively hybridize to mRNAs transcribed from a transcription unit of genome, useful for detecting tissue-, pathology-, and developmentalspecific genes.

Example 1; SEQ ID NO 10766; 47pp; English.

\$XXCCCCCCCCCCCCCCCCCX

The present invention describes oligonucleotide libraries for detecting messenger RNAs that populate a (sub-)transcribtome, where the (sub-)transcriptome comprises messenger RNAs transcribed from multiple transcription units that populate a genome. The library comprises several oligonucleotides, each capable of hybridising selectively to a set of messenger RNAs transcribtion unit of the genome, which encodes one or more messenger RNA splice variants. The coligonucleotide libraries are useful for detecting mRNAs from a coligonucleotide libraries are useful for detecting mRNAs from a coligonucleotide libraries and splice variants of human or animal cranscriptomes. The libraries may also be used as specialised minicatoriptomes. The libraries may also be used as specialised minicatoriptomes. The libraries may also be used as specialised minicatoriptomes. The libraries of a sub-transcriptome under a particular biological cranscriptes of a sub-transcriptome under a particular condition; to detect or appecific genes such as those genes only expressed in specific pathological condition; to detect or variants of a transcriptome of a patient suffering from a particular disorder. ABN27253 to ABN59589 represent oligonucleotide sequences from a particular invariant of a transcriptome of a patient suffering from a particular for area, hunds are used in the exemplification of the present invention. N.B. The sequence data for this patent did not form part of the printed specification, but was obtained in electronic format directly from WIPO at ftp.wipo.int/pub/published\_pct\_sequences

Sequence 60 BP; 19 A; 17 C; 13 G; 11 T; 0 U; 0 Other;

00000 Length:
Matches:
Conservative:
Mismatches: Gaps: 644 102.00 100.00% 100.00% 1.63% Percent Similarity: Best Local Similarity: Alignment Scores: Query Match: Pred. No.:

US-09-674-237B-3 (1-1213) x ABN38018 (1-60)

ACN59557 standard; cDNA; 99 ACN59557/c RESULT 3

BP.

ACN59557;

02-DEC-2004 (first entry)

Cotton gynoecium tissue EST Clone ID: LIB3829-032-Q6-N6-F4, SEQ:14338.

Cotton; plant; EST; expressed sequence tag; transgenic plant; gynoecium; variety Nucotton33B; library LIB3829; molecular tag; molecular marker; genetic mapping; molecular mapping; seed germination; plant growth; plant quality; plant yield; plant breeding; tissue printing; 88.

8X8X4X4X4X4X

Gossypium hirsutum

US2004123340-A1.

OM protein

Run on:

Sequence:

```
Acn5955 Cotton gy
Acn5954 Cotton gy
Acn59315 Cotton gy
Aai84741 Human pol
Acn59545 Cotton gy
Abv89298 Human pol
Acn5966 Self-coal
Acn336166 Self-coal
Acn336166 Self-coal
Acn3316 Human gen
Acn70530 Human gen
Ach70530 Human gen
Ach70530 Human gen
Ach70530 Human gen
Ach70530 Human gel
Ach70530 Human gel
Ach8058 HVR1 regi
Ach8058 HVR1 regi
Ach8058 Human gel
Ach8058 Human gel
Ach8058 Human gel
Ach8058 Candida a
Ach8058 Candida a
Acc56406 Oligonucl
Ach8058 Luman gen
Ach8058 Human gel
Ach8058 Human gel
Ach8058 Human gel
Ach8058 Human gel
Ach8058 Candida a
Acc56406 Oligonucl
Ach8058 Luman gen
Ach8058 Luman gel
Ach8058 Luman gel
Ach8058 Luman gel
Ach8058 Human gel
Ach8058 Luman gel
Ach8058 Candida a
Acc56406 Oligonucl
Acc65406 Oligonucl
Acc65406 Oligonucl
Acc65406 Oligonucl
Acc65406 Oligonucl
Acc65406 Oligonucl
Acc65406 Oligonucl
                                                                                                                                                                                                                                                                                                                                                                                                                                                         Ach46043 Cotton pr
Ach59546 Cotton gy
Aa184826 Human pol
Ad160206 Rat cDNA
Ad136167 Self-coal
Ach88910 Human gen
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 Aac65406 Oligonucl
Aac65407 Oligonucl
Aaq33526 Sequence
Aaz57144 Exemplary
Ach89206 Human gen
Aaq62559 Candida a
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               Oligonuclectide array, useful for measuring ortholog gene-expression distribution, comprising number of oligonuclectides derived from ortholog
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   oligonuclectide array; orthologue; homology; expression distribution; change; gene-expression; rat; probe; ss.
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Abn57047 M
Abn54472 M
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                                                                                        ACN59545
ACN61067
ABV89298
ADJ36166
AAC14094
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AAT23132
ADH70530
                                                                                                                                                                                                                                                                        ABN39460
AAI84742
ABN35290
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AAF18418
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     WPI; 2004-113862/12.
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     Adp49483 Oligonucl
Abn38018 Human spl
Acn59557 Cotton gy
Acn59485 Cotton gy
Acn46027 Cotton py
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                                                                                                                                                                                                                 6269
1 MAQFPTPFGGSLDVWALTVE.....VGLFPSNYVKLTTDMDFSQQ 1213
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                                                                                                                        April 28, 2005, 20:56:09 ; Search time 1397 Seconds
                  GenCore version 5.1.6
Copyright (c) 1993 - 2005 Compugen Ltd.
                                                                                      - nucleic search, using frame plus p2n model
                                                                                                                                                                                                                                                                                                                                                                                                               of hits satisfying chosen parameters:
                                                                                                                                                                                                                                                                                                                                                                               4390206 seqs, 2959870667 residues
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ACN59485
ACN46027
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ABN38018
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Xgapop 10.0 , Xg.
Ygapop 10.0 , Ygapex.
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"rapop 6.0 , Delext
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Total number

Searched:

Score

Result

155 102 89 84 79

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Perfect score:

Sequence:

1

OM protein

Run on:

Scoring table:

Searched:

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http://baygenomics.ucsf.edu/
http://baygenomics.ucsf.edu/
Unpublished (2001)
Contact: BayGenomics
Bay Area Functional Genomics Consortium (BayGenomics)
Bay Area Functional Genomics.ucsf.edu
Bemail: info@baygenomics.ucsf.edu
Sequence tag generated by 5' RACE of total RNA from gene trap ES
cell line. ES cell lines harboring insertion mutation of target
gene are available upon request from BayGenomics. Annotation
information available from
http://baygenomics.ucsf.edu/cgi-bin/BaySearch.py?OPTION=EXACT&TYPE=
CELL_LINE&KEY=XE464
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               GSS 09-MAY-2003
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CK876555 SGF13924
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CV295974 ESTB84351
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CV295974 ESTB84751
CR459729 929944 MA
CV296344 ESTB84721
BE662207 BJ166-Y
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CK918229 VVD030C08
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CC901776 BJ02017A0
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Mammalia; Eutheria; Rodentia; Sciurognathi; Muridae; Murinae; Mus.
1 (bases 1 to 94)
BayGenomics.
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CB918229
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Location/Qualifiers
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Mus musculus
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CC199586.1 GI:30479626
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AUTHORS
TITLE
JOURNAL
COMMENT
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CC199586
LOCUS
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AV963382 AV963382
CK891128 SCP163390
CB262655 53 R8866-
AL821665 AL821665
AUS50968 AUZ50968
AW691901 NF05E015
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AA589590 v149c09.s
AV963382 AV963382
                                                                                          April 28, 2005, 22:12:55 ; Search time 8531 Seconds (without alignments) 5412.256 Million cell updates/sec
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                                                                                                                                                                           MAQFPTPFGGSLDVWAITVE.....VGLFPSNYVKLTTDMDPSQQ 1213
               GenCore version 5.1.6
Copyright (c) 1993 - 2005 Compugen Ltd.
                                                                  nucleic search, using frame_plus_p2n model
                                                                                                                                                                                                                                                                                       34239544 segs, 19032134700 residues
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AA589590
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CR262655
ALB2665
AU250968
AW691901
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Ygapop 10.0 , Ygapext
Fgapop 6.0 , Fgapext
Delop 6.0 , Delext
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90-htc::

90-est3::

90-est5::

90-est5::

90-gs81::
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Match Length
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1099 LysAsnProGlyGlyTrpTrpGluGlyGluLeuGlnAlaArgGlyLysLysArgGlnIje 1118
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                                                                                                                                                                                                                                                                                                                                                                                AV963382 Nori Satoh unpublished cDNA library, egg Ciona integrinalis cDNA clone cieg21112 5', mRNA sequence.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           Eukaryota, Metazoa, Chordata, Urochordata, Ascidiacea, Enterogona, Phlebobranchia, Cionidae, Ciona.

1 (bases 1 to 99)
Satoh, N., Satou, Y., Kohara, Y. and Shin-i, T.

Expressed genes in Ciona intestinalis
                                                                                                                                                                                                                                        2 GCCATGTACACATACGAGAGTTCTGATCAAGGAGATTTAAAGTTTCAGCAAGGGGATGTG 61
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Conservative:
Mismatches:
Indels:
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Sakyo-ku, Kyoto, Kyoto 606-8502, Japan
Tel: 81-75-753-4081
Fax: 81-75-705-1113
Fmail: satch@ascidian.zool.kyoto-u.ac.jp.
Location/Qualifiers
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Matches:
Conservative:
Mismatches:
Indels:
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Department of Zoology
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Ciona intestinalis
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VERSION
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ORGANISM
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                                                                                                                                                                                                                                                                                                                                                                                        LOCUS
DEFINITION
                                                                                  Pred. No.:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               AUTHORS
TITLE
JOURNAL
COMMENT
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AV963382
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                                   DRIGIN
                                                                                                      Score:
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                                                                                                                                                                                                                                                                                              à
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      /tissue type="whole skin"
/dev_stage="11 weeks old"
/dev_stage="11 weeks old"
/dab host="50LR (kanamycin resistant)"
/clone lib="Stratagene mouse skin (#937313)"
/note="Organ: skin; Vector: pBluescript SK-; Site_1:
/note="Organ: skin; Vector: pBluescript SK-; Site_1:
/note="Organ: skin; Time mouse skin from li week old C57BL/6 female mice.
Average insert size: 1.0 kb; Uni-ZAP XR Vector; -5'
                                                                                                                                                                                                                                                                                                                                                                                                      AA589590 T49-1997 AA6909.sl Stratagene mouse skin (#937313) Mus musculus cDNA clone INAGE:975568 3' similar to SW:YFJ4_YEAST P43603 HYPOTHETICAL 40.4
                                                                                                                                                                                                                                              210 ProproAlaAlaGluTrpAlaValProGlnSerSerArgLeuLysTyrArgGlnLeuPhe 229
                                                                                                                                                                                                                                                                 This clone is available royalty-free through LLNL; contact the IMAGE Consortium (info@image.llnl.gov) for further information. MGI:556296
   /cell_type="Bmbryonic stem cell"
/clone_lib="BayGenomics Gene Trap Library pGTlLxf"
/note="Vector: pGTlLxf"
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                The WashU-HMMI Mouse BST Project
Unpublished (1996)
Contact: Marra M/Mouse BST Project
WashU-HHMI Mouse EST Project
WashIngton University School of MedicineP
444 Forest Park Parkway, Box 8501, St. Louis, MO 63108
Tel: 314 286 1800
Email: mouseest@watson.wustl.edu
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          Possible reversed clone: similarity on wrong strand Seq primer: -28ml3 revl ET from Amersham High quality sequence stop: 1. Location/Qualifiers
                                                                                                      94
                                                                                                   Length:
Matches:
Conservative:
Mismatches:
Indels:
                                                                                                                                                                                                                                                                                                              230 AsnSerHisAspLysThrMetSerGlyHisLeu 240
                                                                                                                                                                                                                                                                                                                                    61 AACAGCCACGACAAAACTATGAGTGGACACTTA 93

    .79
    /organism="Mus musculus"
/mol_type="mRNA"
    /strain="C57BL/6"

                                                                                                                                                                                     Gaps:
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clone="IMAGE:975568"
                                                                                                                                                                                                                    (1-94)
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     Mus musculus (house mouse)
Mus musculus
                                                                                                                                                                                                                    US-09-674-237B-3 (1-1213) x CC199586
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            sex="females"
                                                                                                                                                                                                                                                                                                                                                                                                                                                                       AA589590.1 GI:2402970
                                                                                                    0.00165
168.00
100.00%
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Best Local Similarity:
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DB:
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AA589590
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AUTHORS
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                                                         DRIGIN
                                                                                                                          Score:
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49

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//LOUGE=WELLE-MILLS-WINDS
//LOUGE=WELLE-MILLS-WINDS
//LOUGE=WELLE-MILLS-WINDS
XhoI; cDNA library from Arabidopsis thaTiana, accession
C24; seedling; Lambda ZAPII phage library was made at the
Max-Planck-Institute of Molecular Plant Physiology, Golm,
Germany and mass-excised at the Max-Planck-Institute for
Plant Breeding Research, Cologne, Germany; cloning sites
BCORI-XhoI; Note: Sequencing granted in the context of the
GABI Arabidopsis Verbund I: Genetic Diversity,
'Establishment of high-efficiency SNP-based mapping tools
and development of methods for genome-wide mutation
detection' PI: Bernd Weisshaar Sequence submission managed
by RZPD/GABI-Primary database: http://gabi.rzpd.de This
clone is available from RZPD; contact RZPD (clone@rzpd.de)
Mitchell-Olds, T. and Weisshaar, B.
Large-scale identification and analysis of genome-wide
single-nucleotide polymorphisms for mapping in Arabidopsis thaliana
Genome Res. 13 (6), 1250-1257 (2003)
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              96 bp mRNA linear EST 15-JUL-2002
ALS21665 N:130 Triticum aestivum cDNA clone AOS_N130_plate_42, mRNA
AL821665
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   394 GluArgGluArgGlnGluGluGluAlaLysArgGlnLeuGluLeuGluLysGlnLeuGlu 413
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             Eukaryota, Viridiplantae, Streptophyta, Embryophyta, Tracheophyta,
Spermatophyta, Magnoliophyta, Liliopsida, Poales, Poaceae,
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         Breeding Research
                                                                                                                                          ADIS DNA core facility at MPIZ
Max-Planck-Institute for Plant Breeding Resear
Carl-von-Linne Weg 10, 50829 Koeln, Germany
Fax: 00492215062851
Bmail: weisshaa@mpiz-koeln.mpg.de
Insert Length: 98 Std Brror: 0.00
Plate: 15 row! G Golumn: 11
Seq primer: pBl2; GGTGGCGGCCCTCTAG.
Location/Qualifiers
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   414 LysGlnArgGluLeuGluArgGlnArgGluGluGluArg 426
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17
119
11
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/tissue_type="seedling"
/dev_trage="few_days_old_seedlings"
/lab_host="E._coli_XL1-Blue_MRF"
/clone_lib="MPIZ-ADIS-008"
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    Conservative:
Mismatches:
Indels:
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Matches:
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/db xref="taxon:3702"
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 Triticum aestivum (bread wheat)
Triticum aestivum
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          US-09-674-237B-3 (1-1213) x CB262655 (1-98)
                                                                                                                                                                                                                                                                                                                                                                         /mol_type="mRNA"
/ecotype="C24"
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            AL821665.1 GI:21833434
EST.
                                                                                                                           Contact: Weisshaar B
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87.50
78.79%
57.58%
1.40%
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Query Match:
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AL821665
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         98 bp mRNA linear EST 06-NOV-2003
Clone MPIZp767G1115Q 5-PRIME, mRNA sequence.
CB262655.1 GI:32887428
EST.
                                             SGP163390 Atlantic salmon Ovaries cDNA library Salmo salar cDNA clone KG4-0756, mRNA sequence.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          Arabidopsis thaliana
Eukaryota; Viridiplantae; Streptophyta; Embryophyta; Tracheophyta;
Spermatophyta; Magnoliophyta; eudicotyledons; core eudicots;
rosida; eurosida II; Brassicales; Brassicaceae; Arabidopsis.
1 (bases 1 to 98)
Schmid,K.J., Soerensen,T.R., Stracke,R., Torjek,O., Altmann,T.,
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    413 GluLysGlnArgGluLeuGluArgGlnArgGluGluGluArgArgLysGluIleGluArg 432
                                                                                                                                                                                                                          Bukaryota; Metazoa; Chordata; Craniata; Vertebrata; Buteleostomi;
Actinopterygii; Neopterygii; Teleostei; Buteleostei;
Protacanthopterygii; Salmoniformes; Salmonidae; Salmo.
1 (bases 1 to 99)
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             /tissue_type="Ovaries"
/dev_stage="Pre-smolt"
/lab_host="XL 10-Gold"
/clone_lib="Atlantic salmon Ovaries cDNA library"
/note="Vector: pBluescript II SK (+) XR; Site_1: EcoRI; Site_2: XhoI"
                                                                                                                                                                                                                                                                                                                                    Expressed Sequence Tags from an Atlantic salmon ovaries cDNA
                                                                                                                                                                                                                                                                                                                                                                                            Contact: Bjorn Hoyheim
Department of Basic Sciences and Aquatic Medicine
Norwegian School of Veterinary Science
DO Dox 8140 DEP, NO-0033 Oslo, Norway
Tel: 47 22 96 47 03
Fax: 47 22 96 47 58
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       433 ArgGluAlaAlaLysArgGluLeuGluArgGlnArgGln 445
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7 7
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    /organism="Salmo salar"
/mol_type="mRNA"
/db_xref="taxon:8030"
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           US-09-674-237B-3 (1-1213) x CK891128 (1-99)
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        Email: Bjorn.Hoyheim@veths.no.
Location/Qualifiers
                                                                                                                                                                                     Salmo salar (Atlantic salmon)
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   /clone="KG4-0756"
                                                                                                                                            CK891128.1 GI:45320861
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72.73%
51.52%
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               66. .1
                                                                                                                                                                                                             Salmo salar
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Best Local Similarity:
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CB262655
                                         CK891128
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/tissue_type="Stem"
/clone_lib="ST"
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AW691901.2 GI:11931888
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53.12%
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87.00
71.88%
53.12%
1.39%
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Best Local Similarity:
Query Match:
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Pred. No.:
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VERSION
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DEFINITION
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AW691901
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  AU250968 ST Lolium multiflorum cDNA clone ST007E06-5, mRNA sequence.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       Eukaryota, Viridiplantae, Streptophyta; Embryophyta; Tracheophyta; Spermatophyta; Magnoliophyta; Liliopsida; Poales; Poaceae; Pooideae; Poeae; Lolium.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    Email: sikeda67@jfsass.or.jp
contact:Tadashi Takamizo (takamizo@affrc.go.jp)
National Institute of Livestock and Grassland Science, Nishinasuno
Resistance gene analog:
Location/Qualifiers
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             413 GlulysClnArgGluLeuGluArgGlnArgGluGluGluArgArgLysGluIleGluArg 432
Pooideae; Triticeae; Triticum.
1 (bases 1 to 96)
Wilson,I., Beswick,R., Shepherd,S., Barker,G., Parker,J., Owen,P.,
Walson,I., Coghill,J., Holdsworth,M., Lenton,J., Shewry,P. and
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               Edwards.K.
A BBSRC-funded wheat EST resource for the academic community Unpublished (2002)
Contact: Barker G
Institute of Arable Grop Research
Long Ashton, Bristol BS41 9AF United Kingdom.
Location/Qualifiers
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   John wultiflorum EST Project Unpublished (2004)
Contact: Seishi Irkeda
Contact: Seishi Irkeda
Copac Green Green Farming Forage Seed Association (JFSA)
Forage Crop Research Institute (FCRI)
Higasiakada 388-5, Nishinasuno, Tochigi 329-2742, Japan Fat: 81-287-37-6755
Fax: 81-287-37-6755
                                                                                                                                                                                                                                       /db_xref="taxon:4565"
/clone="A05_N130_plate_42"
/tissue_type="embryo"
/dev_stage="2 days post germination"
/clone_lib="N:130"
                                                                                                                                                                                                                                                                                                                                                                    96
17
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9
0
                                                                                                                                                                                                                                                                                                                                                                 Length:
Matches:
Conservative:
Mismatches:
Indels:
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             /organism="Lolium multiflorum"
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/db_xref="texon:4521"
/clone="ST007806-5"
                                                                                                                                                                               1. .96
/organism="Triticum aestivum"
/mol_type="mRNA"
/cultivar="Mercia"
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   Lolium multiflorum (Italian ryegrass)
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Best Local Similarity:
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AUTHORS
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AU250968
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AW691901

97 bp mRNA linear EST 20-DEC-2000
NF050E01ST1F1000 Developing stem Medicago truncatula cDNA clone
NF050E01ST 5', mRNA sequence.
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            He.X.-Z., Shadle,G., Scott,A.D., Harris,A.R., Gonzales,R.A., Bell,C.J., Flores,H.R., Inman,J.T., Weller,J.W., May,G.D. and Dixon,R.B.

Expressed Sequence Tags from the Samuel Roberts Noble Foundation Medicago truncatula stem library Unpublished (2000)
On Apr 14, 2000 this sequence version replaced gi:7566637.
                                                                                                                                                                                               413 GluLysGlnArgGluLeuGluArgGlnArgGluGluGluArgArgLysGluIleGluArg
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/tissue type="stem"
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/clone lib="Developing stem"
/note="Vector: Lambda Zap; Contains a mixture of internodal stem segments"
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              Plant Biology Division
The Samuel Roberts Noble Foundation
2510 Sam Noble Parkway, Ardmore, OK 73402, USA
Fax: 580 221 7380
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                Fax: Dbv cr. ...
Email: radixon@noble.org
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              Insert Length: 826 Std Error: 0.0 plate: 050 row: E column: 01 Seq primer: TCACACAGGAAACAGCTATGAC. Location/Qualifiers
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Medicago truncatula
                                                                                                                Gaps:
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ACCESSION VERSION KEYWORDS

AW693216 RESULT 9

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/note="Vector: pSPORT1; Site 1: Sall; Site 2: Not1; cDNA library from Arabidopsis thaliana, accession Eifel-2; ten week old total plants grown under long-day conditions in soil, whole adult plants were treated for 24 hours with different stresses, (1) at 4M-0 C in the dark, (2), at 37 Grad C in the dark, (3) lying in the lab after removing from soil, (4) in the greenhouse after wounding leaves with a foreceps, (5) in the lab watering with a 150 mM NaCl solution, (6) at 26 M-OC in the light/UV; equal guantities of stressed plant material were pooled; library was made at the Max-Planck-Institute for Plant Breeding Research, Cologne, Germany; cloning sites Sall-Not!, primer sites and orientation:

T7-Sall-CCACGCGTCG-Sprime-cDNA-polyA-CC-Notl-SP6; Note: Sequencing granted in the context of the GABI Arabidopsis Verbund I: Genetic Diversity, 'Establishment of high-efficiency SNP-based mapping tools and development of methods for genome-wide materian development of weisshaar Sequence submission managed by RZDP/GABI-Frimary database: http://gabi.rzpd.de. This clone is available from RZDP; contact RZPD (clone@rzpd.de) for further
                                                                                                                                                                                                                                                           Arabidopsis thaliana (thale cress)
Arabidopsis thaliana
Bukaryota; Viridiplantae; Streptophyta; Embryophyta; Tracheophyta;
Bukaryota; Viridiplantae; Streptophyta; Embryophyta; Tracheophyta;
Benmatophyta; Magnoliophyta; eudicotyledons; core eudicots;
rosids; eurosids II; Brassicales; Brassicaceae; Arabidopsis.
1 (bases I to 97)
Schmid, K.J., Soerensen, T.R., Stracke, R., Torjek, O., Altmann, T.,
Mitchell-Olds, T. and Weisshaar, B.
Large-scale identification and analysis of genome-wide
single-nucleotide polyworphisms for mapping in Arabidopsis thaliana
Genome Res. 13 (6), 1250-1257 (2003)
                                                                                                          CB256469 97 bp mRNA linear BST 06-NOV-2003
77-E010847-027-001-A17-spP2 MPIZ-ADIS-027 Arabidopsis thaliana cDNA
clone MPIZp772A171Q 3-PRIME, mRNA sequence.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  /organism="Arabidopsis thaliana"
/mol_type="manAn"
/mol_type="manAn"
/do_xref="GaBI:59363"
/do_xref="taxon:3702"
/clone="MPIZp772A1710"
/tissue_type="whole plant"
/do_tstage="adult plant,"
/da_hoss="B. coli TOP10"
/clone_ilb="MPIZ-ADIS-027"
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                Contact: Weisshaar B
ADIS DNA core facility at MPIZ
ADIS DNA core facility at MPIZ
MAx-Planck-Institute for Plant Breeding Research
Carl-von-Linne Weg 10, 50829 Koeln, Germany
Fax: 00492215062851
Email: weisshaa@mpiz-koeln.mpg.de
Insert Length: 97 Std Error: 0.00
Insert Length: 97 Std Error: 0.00
Flate: 1 row: A column: 17
Seg primer: spP2; ATTTAGGTGACACTATAGAAGA.
Location/Qualifiers
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                                                                                               413 GluLysGlnArgGluLeuGluArgGlnArgGluGluGluArgArgLysGluIleGluArg 432
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    Eukaryota, Viridiplantae, Streptophyta, Embryophyta, Tracheophyta,
Spermatophyta, Magnoliophyta, eudicotyledons, core eudicots,
rosida, eurosida I, Fabales, Fabaceae, Papilionoideae, Trifolieae,
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                                                                                                                                Expressed Sequence Tags from the Samuel Roberts Noble Foundation Medicago truncatula stem library Mupublished (2000)
On Apr 14, 2000 this sequence version replaced gi:7567952.
Contact: Dixon RA
Plant Biology Division
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He,X.-Z., Shadle,G., Scott,A.D., Harris,A.R., Gonzales,R.A.,
Bell,C.J., Flores,H.R., Inman,J.T., Weller,J.W., May,G.D. and
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/dlome lib="Developing stem"
/note="Vector: Lambda Zap; Contains a mixture of
internodal stem segments"
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  The Samuel Roberts Noble Foundation 2510 Sam Noble Parkway, Ardmore, OK 73402, USA Tel: 580 221 7300
Fax: 580 221 7380
Email: radixon@noble.org
Insert Length: 856 Std Error: 0.00
Plate: OG1 row: F column: 12
Seq primer: TCACACAGGAAACACTATGAC.
Location/Qualifiers
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  Gaps:
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                                               US-09-674-237B-3 (1-1213) x AW691901 (1-97)
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                             AW693216.2 GI:11958379
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JOURNAL COMMENT

TITLE

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AUTHORS REFERENCE

CR580027/c LOCUS DEFINITION ACCESSION VERSION

KEYWORDS

RESULT 11

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REFERENCE AUTHORS TITLE JOURNAL COMMENT

FEATURES

ORIGIN

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Expressed Sequence Tags from an Atlantic salmon gills CDNA library
Unpublished (2004)
Contact: Bjorn Hoyheim
Department of Basic Sciences and Aquatic Medicine
Norwegian School of Veterinary Science
PO Box 8146 DEP, NO-0033 Oslo, Norway
Tel: 47 22 96 47 03
Fax: 47 22 96 47 58
Email: Bjorn:Hoyheim@veths.no.
S
Location/Qualifiers
I. 98
/ mol_type="mRNA"
/ mol_type="mRNA"
/ db_tref="taxon:8030"
/ tion="ground tine="fills"
/ tion="fills"
98 bp mRNA linear EST 09-MAR-2004
G7-0868, mRNA sequence.
CK878555
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BJ02039B01 BJ02 Capsicum annuum CDNA 5', mRNA sequence.
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1 (bases 1 to 30)

Song, W. Y., Jeon, W. B., Kim, K. S., Lee, H. H., Ko, M. K., Kim, Y. S., Hong, J. C. and Oh, B. J.
Generation of Hot Pepper (Capsicum annuum) ESTs (Express Sequence Trags) from Red Ripe Fruit (Song, et al.)
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      413 GlulysGlnArgGluLeuGluArgGlnArgGluGluGluArgArgLysGluIleGluArg 432
                                                                                                                                                                      Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
Actinopterygii; Neopterygii; Teleostei; Euteleostei;
Protacanthopterygii; Salmoniformes; Salmonidae; Salmo.
1 (bases 1 to 98)
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/lab_host="XL 10-Gold"
/clone lib="Atlantic salmon Gills cDNA library"
/note="Vector: pBluescript II SK (+) XR; Site_1: EcoRI;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              98
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Mismatches:
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Salmo salar (Atlantic salmon)
Salmo salar
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Capsicum annuum
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SOURCE
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           CK878555
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                                                                                                                                                                                                                                                                                              CRS80027 CC-tailbud-head Xenopus tropicalis cDNA clone THdA040a23
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       413 GluLysGlnArgGluLeuGluArgGlnArgGluGluGluArgArgLysGluIleGluArg 432
                                                                                                        413 GluLysGlnArgGluLeuGluArgGlnArgGluGluGluArgArgLysGluIleGluArg 432
                                                                                                                                                                                                                                                                                                                                                                                                                                       Eukaryota, Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi; Amphibia; Batrachia; Anura; Mesobatrachia; Pipoidea; Pipidae; Kenopodinae; Kenopus; Silurana.

1 (bases 1 to 97)

1 (bases 1 to 97)

2 coning, M.D.R., Ashurst, J.L., Taylor, R., Garrett, N. and Rogers, J. Sanger Xenopus tropicalis EST project 2001 (2004)
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               /clone="TRACANGO 23"
/clone="TRACANGO 23"
/dev stage="tailbud head (stage 28-30)"
/lab_host="Bscherichia ocoli DH10B."
/clone lib="XGC-tailbud-head"
/note="Vector: pCS107; Site_1: EcoRI; Site_2: NotI; cDNA was oligo dT primed from 5ug of poly A+ RNA from tailbud head. EcoRI-NotI cut cDNA was then ligated into pCS107 with EcoRI the 5' end and NotI at the 3' end."
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               Sanger Institute
Hinxton, Cambridgeshire, CB10 1SA, UK
Bmail: trop@sanger.ac.uk
Sanger Xenopus tropicalis EST project 2001
TROPICALIS_SEQUENCE_ID: THAA040a23.qlkT7
This sequence is from a Xenopus Gene Collection (XGC) library constructed by Nigel Garrett.
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                                                                                                                                                                                433 ArgGluAlaAlaLysArgGluLeuGluArgGlnArg 444
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                                                                                                                                                                                                       Xenopus tropicalis (western clawed frog)
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             organism="Xenopus tropicalis"
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Indels:
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                                                                   US-09-674-237B-3 (1-1213) x CB256469 (1-97)
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Location/Qualifiers
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71.88$
53.12$
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         1.39%
                                                                                                                                                                                                                                                                                                                          3', mRNA sequence.
CR580027
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DB:
           Query Match:
DB:
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Percent Similarity:
Best Local Similarity:
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             CV295974 100 bp mRNA linear EST 23-SEP-2004 SST884351 petunia floral development cDNA library Petunia x hybrida CDNA clone Petunia-DevA-6-F01 5' end, mRNA sequence.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        Bmail: dclark@mail.ifas.ufl.edu
Contact Dr. Clark (dclark@mail.ifas.ufl.edu) for clone information
Seg primer: T3 primer.
Location/Qualifiers
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              Petunia x hybrida
Bukaryota, Viridiplantae, Streptophyta, Embryophyta, Tracheophyta,
Spermatophyta, Magnoliophyta, eudicotyledons, core eudicots,
asterids, lamids, Solanales, Solanaceae, Petunia.
1 (bases 1 to 100)
                                                                                                                                                                                                                                                                 /note="Vector: pBluescript II SK(+)XR; Site 1: EcoRI; Site 2: XhoI; cDNA library was generated from red ripe fruit pericarp using lambda Zap II phage vector. In vivo excision was done with helper phage to generate subclone in pBluescript II SK(+)XR] vector."
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           413 GluLysGlnArgGluLeuGluArgGlnArgGluGluGluArgArgLysGluIleGluArg 432
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              Contact: Boung-Jun Oh
Jeonnam Biotechnology Research Center
Namyang Bld. #603, 10-4 Gwangsan-dong, Dong-gu, Gwangju 501-180,
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  1545 Fifield Hall, Box
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             433 ArgGluAlaAlaLysArgGluLeuGluArgGlnArgGlnLeuGlu 447
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              /db_xref="taxon.4072"
/tissue type="red pepper fruit pericarp"
/clone lib="BJ02"
                                                                                                                                                                                                                                                                                                                                                                                                            165590
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Conservative:
Mismatches:
Indels:
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Environmental Horticulture Department, 1
110670, Gainesville, FL 32611-0670, USA
Tel: 352-392-1831 x370
Fax: 352-392-3870
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        /organism="Petunia x hybrida"
                                                                                                                                                                      organism="Capsicum annuum"
                                                                                                                                                                                                                                                                                                                                                                                                            Length:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   UF floriculture Biotechnology Lab
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                                                                                                                  Location/Qualifiers
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                                                                                                                                                                                    /mol_type="mRNA"
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       /mol_type="mRNA"
                                                                  Tel: 82 62 607 2422
Fax: 82 62 607 6205
Email: bjo@biohub.re.kr
Plate: 039 row: B colu
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Contact: David Clark
                                                                                                                                                                                                                                                                                                                                                                                                          1.74e+03
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68.57%
54.29%
1.37%
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/tissue type="all floral organs"
/tissue type="all floral organs"
/tlab_host="letumada ZAPII unidirectional"
/tlab_host="letumada ZAPII unidirectional"
/clone lib="petunia floral development cDNA library"
/clone lib="petunia floral development cDNA library"
/note="Vector: pBluescript SK-; Site 1: EcoRI; Site 2:
XhoI; supplier: Petunia x hybrida cv. Mitchell Diploid
plants were grown from seeds to a fully flowering stage
under standard greenhouse conditions. Ten entire flowers
of six developmental stages were collected on the same day
from plants grown in standard greenhouse. The flower
stages were as follows in chronological order from
youngest to oldest: stage 1 - no color in corolla;
orolla .75-1 inches long) stage 3 - fully elongated
corolla (not open); corolla 1.5 inches long stage 4 -
fully open corolla; anthers not yet dehisced stage 5 -
fully open corolla; anthers not yet dehisced stage 5 -
fully open corolla; freshly anthesed, bright yellow
pollen; wet stigma stage 6 - pre-senescent; yellowing of
corolla tube; dry brown pollen (if present); stigma dry.
Total RNA was extracted from each sample was combined for subsequent poly
A+ mRNA selection and cDNA synthesis."
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BJ03029F05 BJ03 Capsicum annuum CDNA 5', mRNA sequence.
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Hong,J.C. and Oh,B.J.
Generation of Hot Pepper (Capsicum annuum) EST8 (Express Sequence
'cultivar="Mitchell Diploid (aka. Mitchell, aka W115 in
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 Jeonnam Biotechnology Research Center
Namyang Bld. #603, 10-4 Gwangsan-dong, Dong-gu, Gwangju 501-180,
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    Bukaryota, Viridiplantae; Streptophyta; Embryophyta; Tracheo
Spermatophyta; Magnoliophyta; eudicotyledons; core eudicots;
asterids; lamiids; Solanales; Solanaceae; Capsicum.
(Dases 1 to 90)
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Unpublished (2004)
Contact: Boung-Jun Oh
                                                                                             clone="Petunia-DevA-6-F01"
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Fax: 82 62 607 6205
Email: bjo@biohub.re.kr
Plate: 029 row: F column: 0
Location/Qualifiers
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CO912202.1 GI:51302505
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/note="Vector: pBluescript II SK(+) KR; Site_1: Toricarp using lambda Zap II phage vector: In vivo excision was done with helper phage to generate subclone in pBluescript II SK(+) KR] vector."
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Matches:
Conservative:
Mismatches:
Indels:
Gaps:
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58.62%
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Best Local Similarity:
Query Match:
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Search completed: April 29, 2005, 13:01:47 Job time : 8540 secs

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Title: Perfect score:

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OM protein

Run on:

Scoring table:

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Searched:

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RESULT 1
US-09-281-481A-6/c

| Sequence 6, Application US/09281481A
| Patent No. 6383747
| GENERAL INFORMATION:
| APPLICANT: DAWKINS, ROGER L. and ABRAHAM, Lawrence J.
| TITLE OF INVENTION: GENETIC ANALYSIS
| NUMBER OF SEQUENCES: 22
| CORRESPESPONDENCE ADDRESS:
| ADDRESSEE: SCULLY SCOTT WIRPHY & PRESSER
| STREET: AOO GARDEN CITY PLAZA
| CITY: GARDEN CITY PLAZA
| CITY: GARDEN CITY PLAZA
| COUNTRY: UNITED STATES OF AMERICA
| COMPUTER: IBM PC COMPATIBLE FORM:
| MEDIUM TYPE: Floppy disk
| COMPUTER: IBM PC COMPATIBLE OF AMERICA
| COMPUTER: PLOPPY disk
| COMPUTER: PLOPPY DATA:
| MEDIUM TYPE: PLOPS/MS-DOS
| SOFTWARE: PatentIn Release #1.0, Version #1.25
| CURRENT APPLICATION DATA:
| APPLICATION NUMBER: US/09/281,481A
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                                                                                                        US-09-580-923-14
US-09-866-108A-15688
US-08-136-277-8
US-08-479-403-8
US-08-835-734-8
                                                                                                                                                                                                                        US-08-781-986A-2841
US-09-513-999C-13843
US-08-145-705A-3
US-09-513-999C-31160
US-09-461-697-229
US-08-222-177A-430
US-08-222-177A-430
                                                                                                                                                                                          US-09-579-894-4
US-08-956-171E-2841
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US-08-182-175A-42
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US-08-474-633A-35
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US-08-474-633A-55
US-08-823-771-35
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PCT-US92-06412-46
                                                            US-08-860-038-13
US-08-860-038-14
US-09-580-923-13
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CLASSIFICATION:
PRIOR APPLICATION DATA:
APPLICATION NUMBER: US 203, 271
APPLICATION NUMBER: US 232, 229
FILING DATE: 16-JUL-1997
APPLICATION NUMBER: PK9279 (AU)
FILING DATE: 01-NOV-1991
APPLICATION NUMBER: PK9279 (AU)
FILING DATE: 30-OCT-1992
ATTORNEY/AGENT INFORMATION:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                9279
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REFERENCE/DOCKET NUMBER:
                              -MODEL-frame+_p2n.model -DEV=x1h
-Os-fogn2 1/02PO gpool/US09674237/runat 27042005 182122 2902/app_query.fasta 1.1351
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-OCALIGN=200 -NORM-ext -HEAPSIZE=500 -NINLEN=0 -MAXLEN=100
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-FORD-STARN TIMEOUT=30 -THREADS=1 -XGAPOP=10 -XGAPEXT=0.5 -FGAPOP=6
-FGAPEXT=7 -YGAPOP=10 -YGAPEXT=0.5 -DBLOP=6 -DELEXT=7
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                Sequence 6, Appli
Sequence 7, Appli
Sequence 18169, A
Sequence 19952, A
Sequence 223, App
Sequence 28, Appli
Sequence 5, Appli
Sequence 4, Appli
Sequence 1, Appli
Sequence 1, Appli
                                                                                                   April 29, 2005, 03:08:25; Search time 446 Seconds (without alignments) 4450.232 Million cell updates/sec
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.
                                                                                                                                                                                                       MAQFPTPFGGSLDVWAITVE......VGLFPSNYVKLTTDMDPSQQ 1213
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Sequence
Sequence
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/cgn2_6/ptodata/1/ina/5A_COMB.seq:*
/cgn2_6/ptodata/1/ina/6A_COMB.seq:*
/cgn2_6/ptodata/1/ina/6A_COMB.seq:*
/cgn2_6/ptodata/1/ina/6B_COMB.seq:*
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/cgn2_6/ptodata/1/ina/PCTUS_COMB.seq:*
/cgn2_6/ptodata/1/ina/PCTUS_COMB.seq:*
           GenCore version 5.1.6
Copyright (c) 1993 - 2005 Compugen Ltd.
                                                                          nucleic search, using frame plus p2n model
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US-09-281-481A-7
US-09-281-481A-7
US-09-573-099C-18169
US-09-573-080A-449
US-09-621-976-12952
US-09-621-976-12952
US-08-481-322-28
US-08-281-481A-5
US-08-145-705A-4
US-08-145-705A-3
US-08-145-705A-3
US-08-145-705A-3
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                                                                                                                                                                                                                                                                                                                                        1202784 seqs, 818138359 residues
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  SUMMARIES
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Maximum Match 100%
Listing first 45 summaries
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Delop 6.0
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100
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seq length: 100
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STRANDEDNESS: sir
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                                                                                                                                                                                                                                                                                                                                                                                                                                                               APPLICANT: DAWKINS, ROGER L. and ABRAHAM, Lawrence J. TITLE OF INVENTION: GENETIC ANALYSIS NUMBER OF SEQUENCES: 22 CORRESPONDENCE ADDRESS: ADDRESSEE: SCULLY SCOTT MURPHY & PRESSER
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 ADDRESSER: SCULLY SCOTT MURPHY & PRESSER
STREET: 400 GARDEN CITY PLAZA
CITY: GARDEN CITY
STATE: NEW YORK
COUNTRY: UNITED STATES OF AMERICA
ZIP: 11530-0299
COMPUTER READBLE FORM:
MEDIUM TYPE: Floppy disk
COMPUTER: IBM PC compatible
OPERATING SYSTEM: PC-DOS/MS-DOS
SOFTWARE: PREDLICATION DATA:
APPLICATION NUMBER: US/09/281,481A
                                                                                                                                                                                                                                                                 96
118
0
0
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Matches:
Conservative:
Mismatches:
Indels:
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APPLICATION NUMBER: US/08/893,971
APPLICATION NUMBER: US/08/893,971
APPLICATION NUMBER: US/08/893,971
APPLICATION NUMBER: US/08/2029
FILING DATE: 29-APR-1994
APPLICATION NUMBER: PC7/AU92/00583
FILING DATE: 01-NOV-1991
APPLICATION NUMBER: PC7/AU92/00583
FILING DATE: 30-OCT-1992
ATTORNEY/AGRAT INFORMATION:
NAME: DIGIGLIO, FRANK S
REFERENCE/DOCKET NUMBER: 9279
TELECOMMUNICATION INFORMATION:
TELEPHONE: +516 742 4343
TELEPHONE: +516 742 4343
INFORMATION FOR SEQ ID NO: 7:
SEQUENCE CHARACTERISTICS:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   US-09-281-481A-7/c
; Sequence 7, Application US/09281481A
Patent No. 6383747
; GENERAL INFORMATION:
          TELECOMMUNICATION INFORMATION:
TELEPHONE: +516 742 4343
TELEPHONE: +516 742 436
INFORMATION FOR SEQ ID NO: 6:
SEQUENCE CHARACTERISTICS:
LENGTH: 96 base pairs
TYPE: nucleic acid
STRANDENESS: single
TOPOLOGY: linear
MOLECULE TYPE: DNA
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88.00
76.67%
60.00%
1.40%
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Best Local Similarity:
Query Match:
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CLASSIFICATION:
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Sequence 18169, Application US/09513999C

Sequence 18169, Application US/09513999C

Sequence 18169, Application US/09513999C

Patent No. 6783961

APPLICANT: Dumas Milne Edwards, J.B.
APPLICANT: Dumas Milne Edwards, J.B.
APPLICANT: Duclert, A.
APPLICANT: Duclert, A.
APPLICANT: Duclert, A.
TITLE OF INVENTION: Expressed Sequence Tags and Encoded Human Proteins.
Patent No. 6783961

CURRENT APPLICATION NUMBER: US/09/513,999C

CURRENT FILING DATE: 2000-02-24

PRIOR APPLICATION NUMBER: US 60/122,487

PRIOR PILING DATE: 1999-02-26

NUMBER OF SEQ ID NOS: 36681

SOFTWARE: Patent.pm

SEQ ID NO 18169

LENGTH: 87
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Matches:
Conservative:
Mismatches:
Indels:
                                                                         Length:
Matches:
Conservative:
Mismatches:
Indels:
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65.50
52.63%
42.11%
1.04%
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US-09-513-999C-18169
                                                                           61.5
88.00
76.67%
60.00%
1.40%
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   NAME/KEY: misc_feature LOCATION: 14
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  NAME/KEY: misc_feature
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LOCATION: 45
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           NAME/KEY: misc_feature
; MOLECULE TYPE: DNA
US-09-281-481A-7
                                                                                                           Percent Similarity:
Best Local Similarity:
Query Match:
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Best Local Similarity:
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GENERAL INFORMATION:
APPLICANT: COGENT NEUROSCIENCE, Inc.
APPLICANT: Lo, Donald C.
APPLICANT: Barney, Shawn
APPLICANT: Barney, Shawn
APPLICANT: Portbury, Stuart D.
APPLICANT: Puranam, Kasturi
APPLICANT: Puranam, Kasturi
APPLICANT: Puranam, Kasturi
APPLICANT: Puranam, Kasturi
APPLICANT: APPLICANT: COMPOSITIONS AND METHODS FOR DIAGNOSING
TITLE OF INVENTION: COMPOSITIONS AND TREATING CONDITIONS, DISORDERS, OR DISEASES INVOLVING
TITLE OF INVENTION: CELL DEATH
FILLE REFERENCE: 10001-005-999
CURRENT APPLICATION NUMBER: US/09/461,697
CURRENT APPLICATION NUMBER: 1999-12-14
NUMBER OF SEQ ID NOS: 466
SOUTHARD: PastSEQ for Windows Version 4.0
SEQ ID NO 223
LENGTH: 96
                                                                                                 419 GluargGluArgGluGluGluArgArgLysGluIleGluArgArgGluAlaAlaLysArg 438
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    406 LeuGluLeuGluLysGlnLeuGluLysGlnLysGlnLeuGluArgGlnArgGluGluGlu 425
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NUCLECTIDE AND DEDUCED
AMINO ACID SEQUENCES OF HYPERVARIABLE
REGION 1 OF THE ENVELOPE 2 GENE OF ISOLATES
OF HEPATITIS C VIRUS AND THE USE OF
REAGENTS DERIVED FROM THESE HYPERVARIABLE
SEQUENCES IN DIAGNOSTIC METHODS AND
VACCINES
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                                                             US-09-674-237B-3 (1-1213) x US-09-621-976-12952 (1-82)
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Matches:
Conservative:
Mismatches:
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       Indels:
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               426 ArgArgLysGluIleGluArgArg 433
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                                                                                                                                                                                                                                                                                        Sequence 223, Application US/09461697 Patent No. 6277974
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         ; Sequence 28, Application US/08484322
; Patent No. 6110465
                                                                                                                                                                         439 GluLeuGluArgGlnArg 444
                                                                                                                                                                                                               65 AAGAAAGAGAGAAAGG 82
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64.00
82.14%
39.29%
       1.02%
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CORRESPONDENCE ADDRESS:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           GENERAL INFORMATION:
APPLICANT: BUKH, J.,
APPLICANT: PURCELL, R
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 ORGANISM: Homo sapiens
US-09-461-697-223
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     APPLICANT: PURCELL,
TITLE OF INVENTION:
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 TYPE: DNA
   Query Match:
DB:
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                                                                                                                                                                                                                                                    4: SINGLE COPY GENOMIC HYBRIDIZATION PROBES AND METHOD OF GENERALT
30307
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                OTHER INFORMATION: Description of Artificial Sequence: repetitive sequence found in OTHER INFORMATION: many eutherial genomes. Length of core repeating element is varia; OTHER INFORMATION: ble and is often polymorphi US-09-573-080A-449
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            410 LysGlnLeuGluLysGlnArgGluLeuGluArgGlnArgGluGluGluArgArgLysGlu 429
                       25
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                                                                                 ---GAGAGAWWAAGAGAAAGAGAGAGAAAGAG 19
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12
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APPLICANT: Giordano, J.Y.
TITLE OF INVENTION: ESTS and Encoded Human Proteins.
FILE REFERENCE: GENSET. 054PR2
CURRENT APPLICATION NUMBER: US/09/621,976
CURRENT FILING DATE: 2000-07-21
NUMBER OF SEQ ID NOS: 19335
SOFTWARE: Patent.pm
SEQ ID NO 12952
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   Length:
Matches:
Conservative:
Mismatches:
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Mismatches:
APPLICANT: JOAN, KNOLL
APPLICANT: ROGAN, PETER
TITLE OF INVENTION: SINGLE COPY GENOMIC HYB
FILE REPERENCE: 30307
CURRENT APPLICATION NUMBER: US/09/573,080A
CURRENT FILING DATE: 2000-05-16
NUMBER OF SEQ ID NOS: 479
SOFTWARE: Patentin version 3.0
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        Length:
Matches:
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                Sequence 12952, Application US/09621976
Patent No. 6639063
GENERAL INFORMATION:
APPLICANT: Dumas Milne Edwards, J.B.
APPLICANT: Jobert, S.
                                                                                                                             RESULT 4
US-09-573-080A-449
Sequence 449, Application US/09573080A
Patent No. 6828097
GENERAL INFORMATION:
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65.00
78.26%
52.17%
1.04%
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76.92%
46.15%
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          ORGANISM: Homo sapiens
US-09-621-976-12952
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            61 AGAGAGAGA 69
                                                                                                                                                                                                                                                                                                                                                                                                                            TYPE: DNA ORGANISM: Artificial
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     Percent Similarity:
Best Local Similarity:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  Best Local Similarity:
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                                                                                                                                                                                                                                                                                                                                                                                                          LENGTH: 69
                                                                                             21
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              DNA
                                                                                                                                                                                                                                                                                                                                                                                                                                                                  FEATURE:
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Query Match:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        Pred. No.:
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APPLICATION NUMBER: US/09/281,481A
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83.33%
61.11%
0.96%
                     FILING DATE:
CLASSIFICATION:
PRIOR APPLICATION DATA:
APPLICATION NUMBER: U
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  TOPOLOGY: 1:
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Best Local Similarit
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             Alignment Scores:
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    RESULT 9
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         156 ProProLeuAlaAsnGlyAlaProProValIleGlnProLeuProAlaPheAlaHisPro 175
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      2 CCACCCCATACATCTGGGGGCACCGCCGCATACAGCCTATGGCCTCACCAGCATCTCA
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Fatent No. 6383747
GENERAL INPORMATION:
GENERAL INPORMATION:
APPLICANT:
FILLE OF INVENTION:
GENERIC ANALYSIS
NUMBER OF SEQUENCES:
CORRESPONDENCE ADDRESS:
ADDRESSEE: SCULLY SCOTT MURPHY & PRESSER
STREET: 400 GRADEN CITY PLAZA
CITY: GANDEN CITY PLAZA
STATE: NEW YORK
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       COMPUTER READABLE FORM:
MEDIUM TYPE: Floppy disk
COMPUTER: IBM PC compatible
OPERATING SYSTEM: PC-DOS/MS-DOS
SOFTWARE: Patentin Release #1.0, Version #1.25
CURRENT APPLICATION DATA:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           Conservative:
Mismatches:
Indels:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     176 Ala---AlaThrTrpProLysSerSerPhe 185
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              US-09-674-237B-3 (1-1213) x US-08-484-322-28 (1-96)
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Matches:
                                                                                                                                                                                                                        SOFTWARE: WORDPERFECT 5.1

SOFTWARE: WORDPERFECT 5.1

CURRENT APPLICATION DATA:
APPLICATION NUMBER: US/08/484,322
FILING DATE: June 7, 1995
CLASSIFFCATION: 424
ATTORNEY/AGENT INFORMATION:
NAME: RICHARD W. BORK
RESISTRATION NUMBER: 36,459
REFERENCE/DOCKET NUMBER: 2026-4116US
REFERENCE/DOCKET NUMBER: 2026-4116US
TELECHANICATION INFORMATION:
TELECHANICATION INFORMATION:
TELECHAN: (212) 758-6849
TELEFAX: (212) 751-6849
TELEFAX: (212) 751-6849
TELEFAX: (212) 751-6849
TELECHAN: (212) 751-6849
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                                                                                                              ZIP. 10154
COMPUTER READABLE FORM:
MEDIUM TYPE: FLOPPY DISK
COMPUTER: IBM PC COMPATIBLE
OPERATING SYSTEM: PC-DOS/MS-DOS
MORGAN & FINNEGAN
ADDRESSEE: MORGAN & FIN
STREET: 345 PARK AVENUE
CITY: NEW YORK
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       63.50
64.52%
54.84%
1.01%
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INDIVIDUAL ISOLATE: TS
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     TYPE: nucleic acid
STRANDEDNESS: single
TOPOLOGY: linear
                                                                        NEW YORK
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Best Local Similarity:
Query Match:
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                                                                                                USA
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US-09-281-481A-5/c
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                                                                                                COUNTRY:
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413 GluLysGlnArgGluLeuGluArgGlnArgGluGluGluArgArgLysGluIle 430
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STREET: 660 White Plains Road
CITY: Tarrytown
STATE: New York
COUNTRY: U.S.A.
ZIP: 10591-5144
COMPUTER READABLE FORM:
MEDIUM TYPE: Diskette, 3.5 inch, 1.4 MB storage
COMPUTER: NEC POWETMATE 1 Plus
OPERATING SYSTEM: DOS
SOFTWARE: WOOTDER: DOS
SOFTWARE: WOOTDER: US/08/145,705A
FILING DATE: October 28, 1993
CLASSIFICATION NUMBER: US/08/145,705A
FILING DATE: October 28, 1993
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               APPLICANT: Springer, Wolfgang; Plempel, Manfred;
APPLICANT: Springer, Wolfgang; Plempel, Manfred;
APPLICANT: Lbberding, Antonius
TITLE OF INVENTION: SPECIFIC GENE PROBES AND
TITLE OF INVENTION: INVESTIGATION OF CANDIDA
TITLE OF INVENTION: ALBICANS
TITLE OF INVENTION: ALBICANS
TITLE OF INVENTION: ALBICANS
TOTAL OF ADDRESS:
ADDRESSEE: SPRING HORN KRAMER & WOODS
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       Length:
Matches:
Conservative:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    US-09-674-237B-3 (1-1213) x US-09-281-481A-5 (1-58)
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Indels:
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APPLICATION NUMBER: German P 42 36 708.5
FILING DATE: OCCODER 30, 1992
ATTORNEY/AGENT INFORMATION:
             APPLICATION NUMBER: 05/00/055/71
FILING DATE: 16-UUL-1997
FILING DATE: 29-APR-1994
APPLICATION NUMBER: WS 232,229
FILING DATE: 01-NOV-1991
APPLICATION NUMBER: PCT/AU92/00583
FILING DATE: 01-CT-1992
ATTORNEY/AGENT INFORMATION:
NAME: DIGIGALIO, FRANK S
REFERENCE/DOCKET NUMBER: 9279
TELECOMMUNICATION INFORMATION:
TELECHONE: +516 742 4343
TELEPHONE: +516 742 4366
INFORMATION FOR SEQ ID NO: 5: SEQUENCE CHARACTERISTICS:
LENGTH: 58 base pairs
TYPE: nucleic acid
STRANDENESS: single
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      Gaps:
US/08/893,971
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FELECOMMUNICATION INFORMATION
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             MEDIUM TYPE: Diskette, 3.5 inch, 1.4 MB storage COMPUTER: NEC POWERMATE 1 Plus OPERATING SYSTEM: DOS
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      APPLICANT: Springer, Wolfgang; Plempel, Manfred; APPLICANT: L bberding, Antonius TITLE OF INVENTION: SPECIFIC GENE PROBES AND TITLE OF INVENTION: PROCESSES FOR THE DIAGNOSTIC TITLE OF INVENTION: INVESTIGATION OF CANDIDA TITLE OF INVENTION: ALBICANS NUMBER OF SEQUENCES: 44
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                647 AspAlaGlnArgArgValGlnGluArgAspLysGln 658
                                                                                                                                                                                                                                                                                                                                                                                                         Length:
Matches:
Conservative:
Mismatches:
Indels:
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APPLICATION NUMBER: German P 42 36 708.5
FILING DATE: October 30, 1992
ATTORNEY/AGENT INFORMATION:
          REGISTRATION NUMBER: 33,141
REFERENCE/DOCKET NUMBER: Bayer 8885-KGB
TELECOMMULICATION INFORMATION:
TELEPHONE: (914) 332-1700
TELEPRAX: (914) 332-1844
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               REGISTRATION NUMBER: 33,141
REFERENCE/DOCKET NUMBER: Bayer 8885-KGB
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                E: SPRUNG HORN KRAMER & WOODS
660 White Plains Road
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              Gaps:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   SOFTWARE: WordPerfect 5.1
CURRENT APPLICATION DATA:
APPLICATION NUMBER: US/08/145,705A
FILING DATE: October 28, 1993
CLASSIFICATION: 536
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               Sequence 3, Application US/08145705A Patent No. 5489513 GENERAL INFORMATION:
                                                                                                                                                                                                            ORGANISM: Candida albicans
                                                                                                                                                                                                                                                                                                                                                                                                             8.19e+03
                                                                                                                           INFORMATION FOR SEQ ID NO: 4
SEQUENCE CHARACTERISTICS:
LENGTH: 100 base pairs
TYPE: nucleic acid
STRANDEDNESS: single
TOPOLOGY: linear
                                                                                                                                                                                                                                                                                                                                                                                                                           60.00
75.00$
31.25$
0.96$
Kurt G. Briscoe
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             Kurt G. Briscoe
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           ZIP: 10591-5144
COMPUTER READABLE FORM:
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ADDRESSEE: SPRUNG HO
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Best Local Similarity:
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                                                                                                                                                                                                                                                                                       ANTI-SENSE: NO ORIGINAL SOURCE
                                                                                                                                                                                                                                                                                                                                                                                         Alignment Scores:
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        Query Match:
                                                                                                                                                                                                                                                                                                                                                                                                           No.:
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GENERAL INFORMATION:
APPLICANT: Saverio Carl Palco
APPLICANT: Sharon J. Keeler
APPLICANT: Sharon J. Keeler
APPLICANT: Janet A. Rice
APPLICANT: Janet A. Rice
TITLE OF INVENTION: Synthetic Storage Proteins with Defined Structure Containing Pr
NUMBER OF SEQUENCES: 113
CORRESPONDENCE ADDRESS:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  144 ProProLeuValSerSerValPro-----ProAlaAlaValProProLeuAlaAsnGly 161
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            ---TCTTCTTGGCCT 97
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16
5
6
12
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1007 Market Street
                                                                                                                                                                                                                                                                                                                                               Length:
Matches:
Conservative:
Mismatches:
Indels:
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APPLICATION NUMBER: US/08/182,175A
                                                                                                                                                                                                                                                                                                                                                                                                                                                       Gaps:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              FILING DATE:
CLASSIFICATION: 800
PRIOR APPLICATION DATA:
APPLICATION NUMBER: 07/743,006
FILING DATE: 9 August 1991
ATORNEY/AGENT INFORMATION:
NAME: Linda Axamethy Floyd
REGISTRATION NUMBER: 33,692
REFERENCE/DOCKET NUMBER: BB-1031
TELECOMMUNICATION INFORMATION:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       Sequence 54, Application US/08182175A Patent No. 5559223
                                                                                                                                                           TOPOLOGY: linear MOLECULE TYPE: DNA (genomic) HYPOTHETICAL: NO
                                                                                                                                                                                                                                                                  Candida albicans
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  TELEX: 835420
INFORMATION FOR SEQ ID NO: 54:
TELEPHONE: (914) 332-1700
TELEFAX: (914) 332-1844
                                                                                                                                                                                                                                                                                                                                      1.16e+04
58.00
53.85%
41.03%
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COMPUTER READABLE FORM:
MEDIUM TYPE: Floppy Disk
                                                   INFORMATION FOR SEQ ID NO: 3
SEQUENCE CHARACTERISTICS:
LENGTH: 100 base pairs
TYPE: nucleic acid
STRANDEDNESS: single
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             (302) 892-7949
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              ADDRESSEE: E.I. d
STREET: 1007 Mark
CITY: Wilmington
STATE: Delaware
                                                                                                                                                                                                                                                                                                                                                                               Percent Similarity:
Best Local Similarity:
Query Match:
                                                                                                                                                                                                                       ANTI-SENSE: NO ORIGINAL SOURCE
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                                                                                                                                                                                                                                                                  ORGANISM:
                                                                                                                                                                                                                                                                                                                            Alignment Scores:
Pred. No.:
                                                                                                                                                                                                                                                                                     US-08-145-705A-3
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                                      TELEX:
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Percent Similarity:
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TELEPHONE:
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Pred. No.:
                                                                                                                                                                                                                                                                                                                                                                                                                                          JS-08-474-633A-63
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OTHER
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                                                                                                                                                                                                                                                           /function= "synthetic storage protein
/product= "protein"
                                                                                                                                                                                                                                                                                                               /standard_name= "5.11.11.5"
                                                                                                                                                                                                                                                                                                                                                                                                                       Conservative:
Mismatches:
Indels:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   US-09-674-237B-3 (1-1213) x US-08-182-175A-54 (1-97)
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            CHIMERIC GENES AND
METHODS FOR INCREASING
INCREASING THE LYSINE
AND THREONINE CONTENT
OF THE SEEDS OF PLANTS
                                                                                                                                                                                                                                                                                                                                                                                       Length:
Matches:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         GENERAL INFORMATION:
APPLICANT: E. I. DU PONT DE NEMOURS AND
APPLICANT: COMPANY
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         OPERATING SYSTEM: PC-DOS/MS-DOS
SOFTWARE: MICROSOFT WORD VERSION 2.0C
CURRENT APPLICATION DATA:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          ADDRESSEE: E. I. DU PONT DE NEMOURS
ADDRESSEE: AND COMPANY
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   Sequence 63, Application US/08474633A Patent No. 5773691
                                                                                                                                                                                                                                                                                               'gene= "ssp'
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 CLASSIFICATION: 800
ATTORNEY/AGENT INFORMATION:
NAME: BARBARA C: SIEGELL
REGISTRATION NUMBER: 30,684
REFERENCE/DOCKET NUMBER: BB-1
TELECOMMUNICATION INFORMATION:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               ZIP: 19898
COMPUTER READABLE FORM:
MEDIUM TYPE: FLOPPY DISK
COMPUTER: IBM PC COMPATIBLE
OPPERATING SYSTEM: PC-DOS/MS.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            1007 MARKET STREET
                                                                                             DNA (genomic)
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57.00
47.50%
35.00%
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TITLE OF INVENTION: METH
TITLE OF INVENTION: NOT
TITLE OF INVENTION: AND
TITLE OF INVENTION: OF T
NUMBER OF SEQUENCE: 107
CORRESPONDENCE ADDRESS:
 SEQUENCE CHARACTERISTICS:
LENGTH: 97 base pairs
                                        TYPE: nucleic acid
STRANDEDNESS: double
                                                                                                                         STRAIN: E. coli
CELL TYPE: DH5 alpha
IMMEDIATE SOURCE:
CLONE: 92-2
                                                                                                                                                                                                      FEATURE:
NAMEN KEY: CDS
LOCATION: 2.88
OTHER INFORMATION:
OTHER INFORMATION:
OTHER INFORMATION:
OTHER INFORMATION:
                                                                            linear
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                                                                            TOPOLOGY: line
MOLECULE TYPE: D
ORIGINAL SOURCE:
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DB:
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125 ProLeuThrAlaValAlaProValProMetGlySerIleProValValGlyMetSerPro 144
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Mismatches:
Indels:
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COMPUTER: IBM PC COMPATIBLE
SOFTWARE: MCROSOFT WORD VERSION 2.0C
CURRENT APPLICATION DATA:
FPLICATION NUMBER: US/08/823,771
FILING DATE: 24-M2-1997
CLASSIFICATION: <Unknown>
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    US-09-674-237B-3 (1-1213) x US-08-474-633A-63 (1-97)
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         INCREASING THE LYSINE AND THREONINE CONTENT
                                                                                                                                                                                                                                                                                                                    function= "synthetic
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Matches:
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                                                                                                                                                                                                                                                                                                                                     storage protein
/product= "protein"
/gene= "ssp"
/standard_name=
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ZIP: 19898
COMPUTER READABLE FORM:
MEDIUM TYPE: FLOPPY DISK
                                                                                                                                                                                                                                                                                                                                                                                                         "5.11.11.\overline{5}"
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ADDRESSEE: E. I. DU PO
ADDRESSEE: AND COMPANY
                                                                                                                    63:
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57.00
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302-992-4931
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                                 TELEX: 835420
INFORMATION FOR SEQ ID NO:
SEQUENCE CHARACTERISTICS:
LENGTH: 97 base pairs
                                                                                                       TYPE: nucleic acid
STRANDEDNESS: double
                                                                                                                                                                                            E. coli
E: DH5 alpha
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OTHER INFORMATION
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CLONE: 92-2
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125 ProLeuThrAlaValAlaProValProMetGlySerIleProValValGlyMetSerPro 144
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/product= "protein"
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/standard name= "5.11.11.5"
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Matches:
Conservative:
Mismatches:
Indels:
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APPLICANT: JEFFREYS, Alec J.
APPLICANT: AROUR. John
TITLE OF INVENTION: SIMPLE TANDEM REPEATS
NUMBER OF SEQUENCES: 125
CORRESPONDENCE ADDRESS:
ADDRESSEE: CUSHMAN DARBY & CUSHMAN, L.L.
                    CURRENT APPLICATION DATA:

APPLICATION NUMBER: PCT/US92/06412
FILING DATE: 1922007
CLASSIFICATION: 530
PRIOR APPLICATION DATA:
APPLICATION DATA:
APPLICATION NUMBER: 07/743,006
FILING DATE: 9 August 1991
ATTORNEY/AGENT INFORMATION:
NAME: Linda Axamethy Floyd
REGISTRATION NUMBER: 33,692
REFERENCE/DOCKET NUMBER: BB-1031
TELECOMMUNICATION INFORMATION:
TELECHONE: (302) 992-4929
TELEPHONE: (302) 892-7949
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Patent No. 5843647
     Microsoft Word, 4.0
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  MOLECULE TYPE: DNA (genomic)
ORIGINAL SOURCE:
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ZIP: 20005-3918
COMPUTER READABLE FORM:
MEDIUM TYPE: Floppy disk
                                                                                                                                                                                                                                                                                                                                                                                       TELEFAX: (302) 892-794
TELEX: 835420
INFORMATION FOR EQG ID NO:
SEQUENCE CHARACTER.FSTICS:
LENGTH: 97 base pairs
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         STRAIN: E. coli
CELL TYPE: DH5 alpha
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 TYPE: NUCLEIC ACID
STRANDEDNESS: double
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OTHER INFORMATION
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STATE: D. C.
COUNTRY: U.S.A.
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Best Local Similarity:
Query Match:
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IMMEDIATE SOURCE:
CLONE: 92-2
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    FEATURE:
NAME/KEY: CDS
        SOFTWARE:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           TOPOLOGY:
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Pred. No.:
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| Sequence 54, Application PC/TUS9206412
| Sequence 54, Application PC/TUS9206412
| GENERAL INFORMATION:
| APPLICANT: Sharon J. Keeler
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1007 Market Street
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      Length:
Matches:
Conservative:
Mismatches:
Indels:
                                                                           ATTORNEY/AGENT INFORMATION:
NAME: BARBARA C. SIEGELL
REGISTRATION NUMBER: 30.684
REFERENCE/DOCKET NUMBER: BB-1037-C
TELECOMMUNICATION INFORMATION:
TELEBRONE: 302-992-4931
TELEFAX: 302-773-0164
TELEX: 835420
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           US-09-674-237B-3 (1-1213) x US-08-823-771-63 (1-97)
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MEDIUM TYPE: Floppy Disk
COMPUTER: Macintosh
OPERATING SYSTEM: Macintosh System, 6.0
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                47 ccarcricarcricarcricarcarca----
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SEQUENCE DESCRIPTION: SEQ ID NO: 63:
PRIOR APPLICATION DATA:
APPLICATION NUMBER: 08/474,633
                                                                                                                                                                                                                                                                                                                                                                                                                                                TOPOLOGY: linear
MOLECULE TYPE: DNA (genomic)
ORIGINAL SOURCE:
                                                   FILING DATE: <Unknown>
                                                                                                                                                                                                                                                                                                                                                       LENGTH: 97 base pairs
TYPE: nucleic acid
STRANDEDNESS: double
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              STRAIN: E. coli
CELL TYPE: DH5 alpha
IMMEDIATE SOURCE:
                                                                                                                                                                                                                                                                                                   INFORMATION FOR SEQ ID NO: 63:
SEQUENCE CHARACTERISTICS:
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OTHER INFORMATION:
storage protein
/product= "protein"
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CITY: Wilmington
STATE: Delaware
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Best Local Similarity:
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DB:
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COMPUTER: IBM PC compatible
OPERATING SYSTEM: PC_DOS/MS-DOS
SOFTWARE: Patentin Release #1.0, Version #1.25
CURRENT APPLICATION DATA:
APPLICATION NUMBER: US/08/332,766A
FILING DATE: 01-NOV-1994
FILING DATE: 10-NOV-1994
PRIOR APPLICATION: 435
PRIOR APPLICATION HASE: GB 9326052.9
FILING DATE: 21-DEC-1993
ATTORNEY/AGENT INFORMATION:
NAME: BIRD, Donald J.
REGISTRATION NUMBER: 25,323
ATTORNEY/AGENT INFORMATION:
NAME: BIRD, Donald J.
REGISTRATION NUMBER: 25,323
REFERENCE/DOCKET NUMBER: 25,323
REFERENCE/DOCKET NUMBER: 25,323
REFERENCE/TOCKET NUMBER: 26,326
FELEFAX: (202) 861-3000
FELEFAX: (202) 861-3000
FELEFAX: (202) 822-0944
FELEFAX: (202) 822-0944
FELEFAX: (102) 822-0944
FELEFAX: (1
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Conservative:
Mismatches:
Indels:
Gaps:
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80.77%
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Best Local Similarity:
Query Match:
DB:
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Pred. No.:
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Search completed: April 29, 2005, 13:09:14 Job time : 449 secs

432 ArgArgGluAlaAlaLys 437 :::|||::: 62 AAAAGGAAAGGAATGAAA 79

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413 GluLysGlnArgGluLeuGluArgGlnArgGlu---GluGluArgArgLysGluIleGlu 431 

Sequence 10766, A

Sequence 14266,

Title: Perfect score:

Sequence:

OM protein

Run on:

Scoring table:

Searched:

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Sequence 10766, Application US/09908975
; Sequence 10766, Application US/09908975
; Publication No. US20030165843A1
; GENERAL INFORMATION:
; APPLICANT: WASSERMAN, Alon
; APPLICANT: MINTZ, Bli
; APPLICANT: MINTZ, Liat
; APPLICANT: FAIGLER, Simchon
; TITLE OF INVENTION: OLIGANUCLEOTIDE LIBRARY FOR DETECTING RNA TRANSCRIPTS AND SPLICE N
; TITLE OF INVENTION: OLIGANUCLEOTIDE LIBRARY FOR DETECTING RNA TRANSCRIPTS AND SPLICE N
; TITLE OF INVENTION: THAT POPULATE A TRANSCRIPTOME
; FILE REPERENCE: 36688-005
; CURRENT FILING DATE: 2001-07-20
; PRIOR APPLICATION NUMBER: US 60/287,724
; PRIOR APPLICATION NUMBER: US 60/221,607
; PRIOR FILING DATE: 2000-07-28
; NUMBER OF SEQ ID NOS: 32337
                                                                                                                                                                               Sequence 808, App
Sequence 14335, A
Sequence 1406, A
Sequence 24, Appl
Sequence 14096, A
Sequence 143, Appl
Sequence 113, Appl
Sequence 449, Appl
Sequence 449, Appl
Sequence 223, Appl
Sequence 224, Appl
Sequence 224, Appl
Sequence 224, Appl
Sequence 223, Appl
Sequence 224, Appl
Sequence 22483, Appl
Sequence 22483, Appl
Sequence 22483, Appl
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Sequence 437, App
Sequence 824, App
Sequence 114, App
Sequence 114, App
Sequence 2210, A
Sequence 2220, A
Sequence 27220, A
Sequence 27220, A
Sequence 2725, A
Sequence 6, Appli
Sequence 6, Appli
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 Sequence 63, Appl
Sequence 63, Appl
Sequence 14331, A
Sequence 14331, A
Sequence 13, Appl
Sequence 15684, A
Sequence 27864, A
Sequence 15688, A
Sequence 2841, Appl
                                                                                   1 US-09-908-975-10766
3 US-10-021-323-14338
3 US-10-021-323-14338
3 US-10-021-323-14336
3 US-10-021-323-14335
3 US-10-021-323-14096
3 US-10-021-323-14096
3 US-10-021-323-14096
3 US-10-021-323-14096
3 US-10-021-323-15848
4 US-10-021-323-15848
6 US-09-926-76-223
7 US-09-908-975-1208
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7 US-09-926-975-1208
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6 US-09-908-975-2804
8 US-10-021-323-14331
6 US-09-908-975-2804
8 US-10-021-323-14331
6 US-09-908-975-2804
8 US-09-908-975-2804
8 US-10-021-323-14331
6 US-09-908-975-2804
8 US-09-908-975-2804
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US-10-015-535-8
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                               Length
Query
Match
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                                   Score
                                                                                         RESULT 1
Result
No.
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-MODEL=frame+ p2n.model -DEV=xlh
-MODEL=frame+ p2n.model -DEV=xlh
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-Q=/cgn2 1/USPTO_spool/US09674237/runat_27042005_182123_2929/app_query.fasta_1.1351
-DB=Published Applications_NA -CFMT=fastap -SUFFTX=szlmI00.rnpb -MINMATCH=0.1
-LOOPCL=0 -LOOPEXT=0 -UNITS=bits -GTRAT=1 -END=-1 -MATRIX=blosum62
-TTRANS=human40.cdi -LIST=45 -DOCALIGN=20 - THR_SCORE=pct - THR_NAX=100
-MAXIEN=100 -USER=US09674237_@CGN 1 1767_@runat_27042005_182123_2929 -NCPU=6
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-DEV_TIMEOUT=120 -WARN TIMEOUT=30 -THREADS=1 -KGAPOP=10 -KGAPOR=10 - KGAPOR=6
-FGAPORT=7 -YGAPOP=10 -YGAPORT=0.5 -DELOP=6 -DELEXT=7
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3684.812 Million cell updates/sec
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                                                                                                                                                                                                                                                                                                                                                                  1 MAQFPTPFGGSLDVWAITVE......VGLFPSNYVKLTTDMDPSQQ 1213
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1: /cgn2_6/ptodata/2/pubpna/USO7_PUBCOMB.seq:*
2: /cgn2_6/ptodata/2/pubpna/PCT_NEW_PUB.seq:*
3: /cgn2_6/ptodata/2/pubpna/PCT_NEW_PUB.seq:*
4: /cgn2_6/ptodata/2/pubpna/USO6_PUBCOMB.seq:*
5: /cgn2_6/ptodata/2/pubpna/USO6_PUBCOMB.seq:*
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                                                                                                                                                                               April 29, 2005, 06:53:05; Search time 2004 Seconds
GenCore version 5.1.6
Copyright (c) 1993 - 2005 Compugen Ltd.
                                                                                                                      nucleic search, using frame_plus_p2n model
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        Total number of hits satisfying chosen parameters:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 5642217 seqs, 3043843248 residues
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Maximum Match 100%
Listing first 45 summaries
                                                                                                                                                                                                                                                                                                                                                                                                                                                           , Ygapext
, Ygapext
, Fgapext
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Xgapop 10.0 ,
Ygapop 10.0 ,
Fgapop 6.0 ,
Delop 6.0 ,
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        Minimum DB seq length: 0
Maximum DB seq length: 100
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Database :

2841, Ap 8, Appli

Sequence 2841, Sequence 8, App

SUMMARIES

Score:

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TITLE OF INVENTION: Nucleic Acid Molecules and Other Molecules Associated With TITLE OF INVENTION: Plants FILE REFERENCE: 38-21(52274)B CURRENT APPLICATION NUMBER: US/10/021,323 CURRENT FILING DATE: 2001-112-12 PRIOR APPLICATION NUMBER: US 60/255, 619 PRIOR PLING DATE: 2000-12-14 NUMBER OF SEQ ID NOS: 17880 SEQ ID NO 14266 LENGTH: 96
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            APPLICANT: Feng, Paul C.C.
APPLICANT: Feng, Paul C.C.
APPLICANT: Fincher, Karen L.
APPLICANT: Ziegler, Toodd E.
TITLE OF INVENTION: Nucleic Acid Molecules and Other Molecules Associated With
TITLE OF INVENTION: Plants
FILE REFERENCE: 38-21(52274)B
CURRENT APPLICATION NUMBER: US/10/021,323
CURRENT FILING DATE: 2001-12-12
PRIOR APPLICATION NUMBER: US 60/255, 619
PRIOR FILING DATE: 2000-12-14
NUMBER OF SEQ ID NOS: 17880
SEQ ID NO 808
LENGTH: 88
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            413 GluLysGlnArgGluLeuGluArgGlnArgGluGluGluGluArgArgLysGluIleGluArg 432
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   413 GluLysGlnArgGluLeuGluArgGlnArgGluGluGluArgArgLysGluIleGluArg 432
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                                                                                                                                                                                                                                                                LOCATION: (1)..(96)
OTHER INFORMATION: unsure at all n locations
OTHER INFORMATION: Clone ID: LIB3829-031-Q6-N6-G3
                                                                                                                                                                                                                                                                                                                                                                          Length:
Matches:
Conservative:
Mismatches:
Indels:
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Matches:
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; OTHER INFORMATION: Clone ID: LIB3825-013-Q1-N6-D1
US-10-021-323-808
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US-10-021-323-808/c
Sequence 808, Application US/10021323
Publication No. US20040123340A1
GENERAL INFORMATION:
APPLICANT: Deikman, Jill
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  1.31e+03
79.00
72.73%
51.52%
1.26%
                                                                                                                                                                                       TYPE: DNA
ORGANISM: GOSSYPium hirsutum
FEATURE:
LOCATION: (1)..(96)
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84.00
68.75$
53.12$
1.34$
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Query Match:
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Best Local Similarity:
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Pred. No.:
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                                                                                                                                                                                                                                                                                                                                                                                                            APPLICANT: Feng, Paul C.C.

APPLICANT: Fincher, Karen L.

APPLICANT: Fincher, Karen L.

APPLICANT: Fincher, Todd E.

ITLE OF INVENTION: Nucleic Acid Molecules and Other Molecules Associated With

ITLE OF INVENTION: Plants

FILE REPERBURGS: 38-21(52274) B

CURRENT APPLICATION NUMBER: US/10/021,323

CURRENT FILING DATE: 2001-12-12

PRIOR FILING DATE: 2000-12-14

NUMBER OF SEQ ID NOS: 17880

SEQ ID NO 14338

LENGTH: 99
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           413 GluLysGlnArgGluLeuGluArgGlnArgGluGluGluArgArgLysGluIleGluArg 432
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Matches:
Conservative:
Mismatches:
Indels:
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Matches:
Conservative:
Mismatches:
Indels:
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              TYPE: DNA ORGANISM: Gossypium hirsutum
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102.00
100.00%
100.00%
1.63%
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Fincher, Karen L.
Ziegler, Todd E.
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72.73%
51.52%
1.42%
                                                             TYPE: DNA ORGANISM: Homo sapiens
                                                                                                                                                                                       Percent Similarity:
Best Local Similarity:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  Best Local Similarity:
Query Match:
       SOFTWARE: Patentin
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              US-10-021-323-14266/c
                                                                                               US-09-908-975-10766
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                        SEQ ID NO 10766
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             Alignment Scores:
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APPLICANT:
APPLICANT:
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Sequence 2, Application US/10488936
Sequence 2, Application US/10488936
Publication No. US20050026149A1
GENERAL INFORMATION:
APPLICANT: Reich, Ziv
TITLE OF INVENTION: NUCLEIC ACID CONSTRUCTS CAPABLE OF HIGH EFFICIENCY DELIVERY OF
TITLE OF INVENTION: POLYNUCLEOTIDES INTO DNA CONTAINING ORGANELLES AND METHODS OF UT
TITLE OF INVENTION: SAME
FILE REFERENCE: 27579
CURRENT APPLICATION NUMBER: US/10/488,936
CURRENT APPLICATION NUMBER: 2004-03-16
NUMBER OF SEQ ID NOS: 3
SOFTWARE: Patentin version 3.1
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               Sequence 14096, Application US/10021323
Sequence 14096, Application US/10021323
Publication No. US20040123340A1
Publication No. US20040123340A1
APPLICANT: Deikman, Jill
APPLICANT: Feng, Paul C.C.
APPLICANT: From C.C.
APPLICANT: Trenge Tooler.
TITLE OF INVENTION: Nucleic Acid Molecules and Other Molecules Associated With TITLE OF INVENTION: Plants
FILE REPERRICE: 38-21(52274)B
CURRENT APPLICATION NUMBER: US/10/021,323
                                                                                                                                                                                                                                                                     413 GluLysGlnArgGluLeuGluArgGlnArgGluGluGluArgArgLysGluIleGluArg 432
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                                                                                                                                                                                                                                                                                            ; FEATURE:
; OTHER INFORMATION: Peptide nucleic acid (PNA) recognition sequence
US-10-488-936-2
                                                                                                                                                                                                                                                                                                                                                            433 ArgGluAlaAlaLysArgGluLeuGluArgGlnArgGln 445
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                                                                                                                                                                                                                            US-09-674-237B-3 (1-1213) x US-10-021-323-15706 (1-89)
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Matches:
Conservative:
Mismatches:
Indels:
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Mismatches:
Indels:
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Matches:
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ORGANISM: Artificial sequence
                                                                1,33e+03
79.00
72.73
51.52
1,26%
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77.00
72.73%
51.52%
1.23%
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Query Match:
DB:
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Best Local Similarity:
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      US-10-021-323-15706
                                                                                                                Percent Similarity:
                                                  Alignment Scores:
Pred. No.:
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LENGTH: 88
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DB:
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APPLICANT: Deikman, Jill
APPLICANT: Feng, Paul C.C.
APPLICANT: Fincher, Karen L.
APPLICANT: Ziegler, Todd E.
TITLE OF INVENTION: Nucleic Acid Molecules and Other Molecules Associated With
TITLE OF INVENTION: Plants
FILE REFERENCE: 38-21(5224)B
CURRENT APPLICATION NUMBER: US/10/021,323
CURRENT FILING DATE: 2001-12-12
PRIOR PRILING DATE: 2000-12-14
NUMBER OF SEQ ID NOS: 17880
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 APPLICANT: Feng, Paul C.C.
APPLICANT: Feng, Paul C.C.
APPLICANT: Fincher, Karen L.
APPLICANT: Sincher, Karen L.
APPLICANT: Sincher, Karen L.
APPLICANT: Application Nucleic Acid Molecules and Other Molecules Associated With TITLE OF INVENTION: Plants
TITLE OF INVENTION: Plants
FILE REFERENCE: 38-21(52274)8
CURRENT APPLICATION NUMBER: US/10/021,323
CURRENT FILING DATE: 2001-12-12
PRIOR APPLICATION NUMBER: US 60/255, 619
PRIOR PLICATION NUMBER: US 60/255, 619
NUMBER OF SEQ ID NOS: 17880
SEQ ID NO 15706
LENGTH: 89
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433 ArgGluAlaAlaLysArgGluLeuGluArgGlnArgGln 445
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   433 ArgGluAlaAlaLysArgGluLeuGluArgGlnArgGln 445
                                                                                              28 ------GAGAGAGAGAGAGAGAGAGA 2
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Matches:
Conservative:
Mismatches:
Indels:
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OTHER INFORMATION: Clone ID: LIB3829-029-Q6-N6-B7
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 , OTHER INFORMATION: Clone ID: LIB3829-032-06-N6-F1
US-10-021-323-14335
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    Gaps:
                                                                                                                                                                                              ; Sequence 14335, Application US/10021323; Publication No. US20040123340A1; GENERAL INFORMATION:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              Sequence 15706, Application US/10021323
Publication No. US20040123340A1
GENERAL INFORMATION:
APPLICANT: Deikman, Jill
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    1.33e+03
79.00
72.73$
51.52$
1.26$
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 TYPE: DNA
ORGANISM: Gossypium hirsutum
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                TYPE: DNA ORGANISM: Gossypium hirsutum
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    Percent Similarity:
Best Local Similarity:
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LENGTH: 89
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Sequence 15848, Application US/10021323
; Sequence 15848, Application WS/10021323
; Sequence 15848, Application No. US20040123340A1
; GENERAL INFORMATION:
; APPLICANT: Deliman, Jill
; APPLICANT: Fincher, Karen L.
; APPLICANT: Fincher, Karen L.
; TITLE OF INVENTION: Nucleic Acid Molecules and Other Molecules Associated With
; TITLE OF INVENTION: Plants
; FILE REFERENCE: 38-21(52274)B
; CURRENT APPLICATION NUMBER: US/10/021,323
; CURRENT PILING DATE: 2001-12-12
; PRIOR APPLICATION NUMBER: US 60/255, 619
; RIGHER OF SEQ ID NOS: 17880
; SEQ ID NO 15848
; LENGTH: 76
                                                                    APPLICANT: Feng, Paul C.C.
APPLICANT: Feng, Paul C.C.
APPLICANT: Fincher, Karen L.
APPLICANT: Ziegler, Todd B.
APPLICANT: Ziegler, Todd B.
TITLE OF INVENTION: Nucleic Acid Molecules and Other Molecules Associated With TITLE OF INVENTION: Plants
FILE REPERENCE: 38-21(52274)B
CURRENT APPLICATION NUMBER: US (10/21,323)
CURRENT FILING DATE: 2000-12-12
PRIOR FILING DATE: 2000-12-14
NUMBER OF SEQ ID NOS: 17880
SEQ ID NO 14326
LENGTH: 73
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            409 GluLysGlnLeuGluLysGlnArgGluLeuGluArgGlnArgGluGluGluArgArgLys 428
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113
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; OTHER INFORMATION: Clone ID: LIB3829-031-Q6-N6-C11
US-10-021-323-15848
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Matches:
Conservative:
Mismatches:
Indels:
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Matches:
Conservative:
Mismatches:
Indels:
Gaps:
 Sequence 14326, Application US/10021323
Publication No. US20040123340A1
GENERAL INFORMATION:
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70.00
79.17%
54.17%
1.12%
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70.00
79.17%
54.17%
1.12%
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ORGANISM: Gossypium hirsutum
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ORGANISM: Gossypium hirsutum
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                                                            APPLICANT: Deikman, Jill
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Best Local Similarity:
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Best Local Similarity:
Query Match:
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Pred. No.:
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TITLE OF INVENTION: POLYNUCLEOTIDE ENCODING A NOVEL TRP CHANNEL FAMILY MEMBER, TRP-PL
TITLE OF INVENTION: SPLICE VARIANTS THEREOF
TITLE OF INVENTION: SPLICE VARIANTS THEREOF
CURRENT ENFERSENCE: D0144 NP
CURRENT APPLICATION NUMBER: US/10/153,244
CURRENT APPLICATION NUMBER: US 60/292,599
PRIOR APPLICATION NUMBER: US 60/362,944
PRIOR APPLICATION NUMBER: US 60/362,944
PRIOR APPLICATION NUMBER: US 60/362,944
NUMBER OF SEQ ID NOS: 335
SOFTWARE: Patent In version 3.1
                                                                                                                                                                                                                                                                                                                                                                                                                   407 GlubeuGlubysGlnbeuGlubysGlnArgGlubeuGluArgGlnArgGluGluBlug 426
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              390 GlnGluArglysGluArgGluArgGlnGluGluAlaLysArgGlnLeuGluLeuGlu 409
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Matches:
Conservative:
Mismatches:
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Conservative:
Mismatches:
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US-10-021-323-14096
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CURRENT FILING DATE: 2001-12-12
PRIOR APPLICATION NUMBER: US 60/255, 619
PRIOR FILING DATE: 2000-12-14
NUMBER OF SEQ ID NOS: 17880
SEQ ID NO 14096
LENGTH: 81
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      Sequence 24, Application US/10153244
Publication No. US20030144191A1
GENERAL INFORMATION:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           427 ArgLysGlulleGluArg 432
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                21 GAGAGAGAGAGAGA 4
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73.00
76.92%
53.85%
                                                                                                                 TYPE: DNA
ORGANISM: Gossypium hirsutum
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72.97%
43.24%
1.15%
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Best Local Similarity:
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US-10-021-323-14326/c
                                                                                                                                                                                                                                                                                    Percent Similarity:
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; ORGANISM: Homo
US-10-153-244-24
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LENGTH: 99
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TITLE OF INVENTION: Higher molecular weight entities and uses therefor
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                FILE REFERENCE: 2385978

CURRENT APPLICATION NUMBER: US/10/449,831A

CURRENT FILING DATE: 2003-05-30

PRIOR APPLICATION NUMBER: USSN 60/384878

PRIOR FILING DATE: 2002-05-31

NUMBER OF SEQ ID NOS: 237

SOFTWARE: Patentin version 3.2

LENGTH: 98
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                                                                                                                                                                                                                                                         TYPE: DNA ORGANISM: Neisseria meningitidis
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              28 AGAGAAGAGAAGAGAGAA
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66.00
85.19%
59.26%
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Best Local Similarity:
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Pred. No.:
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                                                                     409 GlulysGlnLeuGluLysGlnArgGluLeuGluArgGlnArgGluGluGluArgArgLys 428
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113
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                     US-09-674-237B-3 (1-1213) x US-10-021-323-15848 (1-76)
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Matches:
Conservative:
Mismatches:
Indels:
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             PRIOR PELICATION NUMBER: PCT/USO1/00666
PRIOR FILING DATE: 2001-01-30
PRIOR PELICATION NUMBER: PCT/USO1/00667
PRIOR PILING DATE: 2001-01-30
                                                                                                                                                                                                                                                                                                                         Sequence 11, Application US/10061201
Publication No. US20030166229A1
GENERAL INFORMATION:
APPLICANT: Shannon, Mark
TITLE OF INVENTION: HUMAN POSH-LIKE PROTEIN
FILE REPERENCE: P801.78
CURRENT APPLICATION VUMBER: US/10/061,201
CURRENT FILING DATE: 2002-01-30
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      9.38e+03
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70.00%
43.33%
1.08%
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                                                                                                                                                                                                                           15 GAGAGAGAGA 4
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Best Local Similarity:
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222768

Length: Matches: Conservative: Mismatches:

Indels:

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US-09-91-867-449

Sequence 449, Application US/09854867

Publication No. US20030224356A1

GENERAL INFORMATION:
GENERAL TOON, FORTER K

TITLE OF INVERTION: SINGLE COPY GENOMIC HYBRIDIZATION PROBES AND METHOD OF GENERATING
TITLE OF INVERTION: US/09/854,867

CURRENT APPLICATION NUMBER: US/09/854,867

CURRENT FILING DATE: 2003-05-08

NUMBER OF SEQ ID NOS: 613

SOFTWARE: Patentin version 3.1

SEQ ID NO 449
                                                                                                                                                                                                                                                                                                                                                    OTHER INFORMATION: Description of Artificial Sequence: repetitive sequence found in OTHER INFORMATION: many eutherial genomes. Length of core repeating element is varia OTHER INFORMATION: ble and is often polymorphic
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       410 LysGlnLeuGluLysGlnArgGluLeuGluArgGlnArgGluGluGluGluArgArgLysGlu 429
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         00200
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               Conservative:
Mismatches:
Indels:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                US-09-674-237B-3 (1-1213) x US-09-854-867-449 (1-69)
                                                                                                                                                                                                                                                                                                                                                                                                                                                                         Length:
Matches:
                                                                                                                                                                                                                                                                                            TYPE: DNA ORGANISM: Artificial Sequence
                                                                                                                                                                                                                                                                                                                                                                                                                                                                    9.52e+03
65.00
78.26%
52.17%
1.04%
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   430 IleGluArg 432
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         61 AGAGAGAGA 69
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                Best Local Similarity:
Query Match:
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63

4 GATATCATCACTGTTCAGCCGAGTGGATGAGAACTGGGGCAGAAGGCAAGTTAGGAGA

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1039 LysSerGlyValPheProSerAsnTyrVal 1048

64 AAAGTAGGCATCTTCCCTATCTTGTA 93

Sequence 113, Application US/10449831A Publication No. US20040029179A1 GENERAL INFORMATION:

US-10-449-831A-113/c

RESULT 13

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APPLICANT: Koentgen, Frank

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RESULT 15

US-10-786-970A-449

US-10-786-970A-449

Sequence 449, Application US/10786970A

Publication No. US20050064449A1

GENERAL INFORMATION:

GENERAL INFORMATION:

APPLICANT: UGAN, KNOLL

APPLICANT: ROGAN, PETER

TITLE OF INVENTION: SINGLE COPY GENOMIC HYBRIDIZATION PROBES AND METHOD OF GENERATING

TITLE OF INVENTION NUMBER: US/10/786,970A

CURRENT APPLICATION NUMBER: US/09/573,080

PRIOR FILING DATE: 2000-05-16

NUMBER OF SEQ ID NOS: 479

SEQ ID NO 449

LENGTH: 69
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            TYPE: DNA
ORGANISM: Artificial
FEATURE:
CHER INFORMATION: Description of Artificial Sequence: repetitive sequence found in
OTHER INFORMATION: many eutherial genomes. Length of core repeating element is varia
CHER INFORMATION: ble and is often polymorphi
US-10-786-9708-449
```

Length:
Matches:
Conservative:
Mismatches:
Indels:

9.52e+03 65.00 78.26% 52.17% 1.04%

Percent Similarity: Best Local Similarity: Query Match: DB:

Alignment Scores:

Gaps:

430 IleGluarg 432 |||||| 61 AGAGAGAGA 69

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Search completed: April 29, 2005, 13:42:45 Job time : 2007 secs